

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 165011

TO: Joseph Woitach

Location: REM/2d51/2c18

Art Unit: 1632 <u>Surf /2</u>, 2005

Case Serial Number: 09/655109

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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CK53466 UI-M-HNO-AY400131 Homo sapi
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/dev_nost="newborn infant"
/lab_nost="E. coli SOLR"
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/note="Corgan: placents; Vector: Uni-ZAP XR; Site_1: EcoR
/note="Corgan: Decorporation of the corgan of the corga

1. .895 /organism="Macaca mulatta"

Location/Qualifiers

/mol_type="mRNA" /strain="Indian" /db_xref="taxon:9544" /sex="male" Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,

Glass

1 (bases 1 to 932) McGuire,K. and Glass, E.J. Unpublished ESTs, McGuire and Unpublished (2004)

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                              Indels
        Score 854.8; DB 7;
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98.8%;
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Best Local Similarity 98.8
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AJ816315
AJ816315 932 bp mRNA linear EST 13-SEP-2004
AJ816315 RN206 Bos sp. cDNA clone C0005210ill, mRNA sequence.
AJ816315
AJ816315.1 GI:51883791
BST.

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 2 AJ816315 LOCUS

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20
                                                           Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the minscore 20 and minmatch 12 options. Vector:pBluesCriptI(SK+) R. Site 1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata.
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Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
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Contact: McGuire K
Genomics and Genetics
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The RIKEN Genome Exploration Research Group Phase II Team and the
                      Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/mol_type="mRNA"
/strain="C57BL/6J"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsunuco, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Matshik, M., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Riken integrated sequence analysis (RISA) system-184-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus 11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:7030405H07 product:RING1 and YY1 binding protein, AK033024
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AGAACCAGAGCTCGGGGTCGGAGAGCACAGACAAGGGTTCCTCCCGCTCCTCCACGC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Haranguk, T., Kasukawa, T., Kaco, K., Kuchara, C., Matsuyama, T., Miyazaki, M., Muranguk, M., Matsuyama, T., Miyazaki, M., Muranguk, M., Makanara, C., Matsuyama, T., Miyazaki, M., Makan, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Shiraki, T., Sano, H., Saaki, D., Shibata, K., Shinagawa, M., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, T., Direct Submission and Hayashizaki, Y.

Direct Submission Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Genome Exploration Research Group, RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Shitter, //genome-gsc.riken.jp, Tel:81-45-503-9216, Comme-gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216, Comme Encyclopedia Project of Genome Exploration Research Group in Riken Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genome Contributed to prepare monse fissues
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Dvrkgtstrkrinsqlvaqqvaqqyatppppkkekkekvekpdkekpekdkdispsv
Tkkntnkktrpksdlikdppseansiqsanattktsetnhtsrprlkknvdrstaqqla
vtvgnvtviitdfkektrssstssstvtssagseqqnqsssgsbstdkgssrsstpkg
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                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1436)
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protein (MGD|MG1:1929059, GB|NM_019743, evidence: BLASTN,
The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                  Liang, F.,
                       Stone, R.T.
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                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
Do Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Small: smith@email.marc.usda.gov
Single pass sequenting. Bases called with phred v0.020425.c and
trimmed with the and of the trim_alt option. Vector identified w
cross match v0.990329.
Plate: 105 row: P column: 12
Plate: 105 row: P column: 12
Seq primer: GTAATACGACTATAGGG.
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1 (bases 1 to 799)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Hacton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine (libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Best Local Similarity 94.9%; Pred. No. 2.3e-182;
Matches 758; Conservative 1; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="pooled"
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/clone lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
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/db_xref="taxon:9913"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                CGATGTGCGGAAAGGCACCTCCACCAGGAAACCTCGCATCAATTCTCAGCTGGTGGCACA
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      TTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTTAAATGCAGCATCTG
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDNA
sequence: 1-23, AMT_rich#Low_complexity
Seg primer: M13 PORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:960"
/clone="Ul-CF-EC1-acc-m-16-0-UI"
/tissue_type="Lung"
/dev stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="Ull-CF-EC1"
/clone_lib="Ull-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 20-FEB-2003
                                                   715
                                                                                                                                                    GCACCCCCCGGGAAATTTTCTGTGGACATCGACCTTTTAGTGATGCTGCCAGGATAATTT 140
                                                                                                                                                                                         834
                                                                                   AATTGTGAAAACTATGAATCAGGGTATGAAATTCACGTCCTCCACCTGCCCATGCTGCTT 200
                                                                                                                   774
                                                                                                                                                                                                                                                           CTTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATCATTTATAATTGGATGTGC 894
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Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
TIGCTIGCCAIGGGCATTIGGCCACCAAGAATTICGCACCCTGACGATACTCTIGACA
                                                                                                                                                                                                                                                                             CITITATGIATICCATIGITITIATATGATITICCIAACAACATITATAAATIGGAIGIGC
                                                                                                                       GCA-TCCCTGGAGAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTT
                                                                                                                                                                                         CTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACA
                                                   AATTGTGAAAACTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               BM985193 736 bp mRNA linear EST 20-FI UI-CF-EC1-acc-m-16-0-UI-S1 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-acc-m-16-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                 TCCTGAATCTACTTTTAT 913
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TITLE
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UI-CF-EC1 is a normalized cDNA library containing the following tissue(8): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) 18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG ITSUE-Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383

TAG LIB-UI-CF-EC1

TAG_SEQ=AAGTGCTTAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            726 AAAGTGAAAAGCAGGACAAAGAGAAACTTGAGAAAGACAAGGAAATTAGTCCTAGTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 CCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCCTCCTA
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Pred. No. 6.7e-179;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.2%;
Best Local Similarity 99.4%;
Matches 713; Conservative
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745 540 805 9 865 9

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: 120 row: A column: 12
Plate: 120 row: A column: 12
Seq primer: GTAARGACTACTARAGGG.
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                         361 GAGAGCACACACACACGCCTCCTCCTCCACGCCAAAGGGCGACATGTCAGGAGTA 420
                                                                                                                                                  421 AATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 726)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wary, J.D., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/lab_host="DH10B"
/clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, thymus, semitendonous muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                          686 ATTCAAAACCTCCACCTGCCCATGCTTGCATCCTGGAGAATCTTCTGTGGACATCG
                                                                                                                                                                                                                                                                                                  746 ACCICITAGIGAIGCIGCCAGGAIAATIICIGCIIGCCAIGGGCAICIGGCCACCAAGGA
                                                                                                                                                                                                                                                                                                                            806 ATTICGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                601 ATTTCGCACCCTGACAATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGATTT
                                                                                                 626 AATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CK777039 1inear 726 bp mRNA linear 964031 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.
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/db_xref="taxon:9913"
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Bos taurus
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/db xref="taxon:9823"
/db xref="taxon:9823"
/clone="scan001dd.dc.20"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
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/clone_lib="sus Scrofa library (scan)"
/clone_lib="sus Scrofa library (scan)"
/note="fissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
BX924636

T07 bp mRNA linear EST 07-MAY-2004
BX924636 Sus Scrofa cDNA clone
scan0017d.d.20 5prim, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAATCACACC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 TCATCCACAGTGACCTCCAGTGCAGGTCAGAACAGCAGAACCAGASCAGCTCGGGGTCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Faxi: 33 (0) 5.61.28.53.08

Faxi: 34 (0) 5.61.28.53.08

Faxi: 34 (0) 5.61.28.53.08

Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 707)
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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1. .707
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                               Contact: Tosser-Klopp G
                                                                                                    BX924636.1 GI:41141484
                                                                                                                                                     Sus scrofa (pig)
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                                                                             ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                      REFERENCE
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Gapser Strausberg, Ph.D.
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.B. Consortium/LiNU at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-23, AT_rich#Low_complexity
Seq primer: MIS FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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UI-H-ED1-axw-f-13-0-UI.81 NCI CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5834508 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                         TGAAAGATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCA 368
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                    667
                                                                                                                                                                                                                                                                      607
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                                                                                                                                                                  AGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAAAGACTGAGAAAGACAAGGAAA
                                                                Gaps
                                                                1;
          Length 726;
                                                              36; Indels
          Score 656; DB 7; I
Pred. No. 5.5e-164;
1; Mismatches 36;
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                  69.3%;
94.8%;
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                  Query Match 69.3
Best Local Similarity 94.8
Matches 688; Conservative
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113 TGACGATTACTCTTGACACCTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATC
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Best Local Similarity 99.2%;
Matches 639; Conservative
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375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
781: 319 335 9256
Fax: 319 335 9266
Fax: 319 335 9265
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Greg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
cDNA - Sequencing by: Dr. M. Bento Soares, University of Iowa
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sequencing by: Dr. M. Bento Soares
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="U1-E-B1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-E-E31 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 15-DEC-2003
                                                                                                   242 TCAAAACCTCCACCTGCCCATGCTTGCATCCCTGGAGAATCTTCTGTGGACATCGAC 183
                                                                                                                                                                                                             CTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAAT 123
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TGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAAAT 243
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK299391 664 bp mRNA linear EST 15-
UI-E-EJI-ajv-e-08-0-UI.sl UI-E-EJI Homo sapiens cDNA clone
UI-E-EJI-ajv-e-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAACAATCATTTATAAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAAAA 10
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Coordinated Laboratory for Computational Genomics
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/organism="Homo sapiens"
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with Not I. and cloned directionally into pT73-P25 vector. The oligonucleotide used to prime the synthesis of first-strand contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATAGCGAT; eye anterior segment, AATGCGCAT; optic nerve, CCATAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_LIB-UIL-E-EJJ TAG_SEQ-AGAATCAAGA"
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stranded cDNA was ligated to an EcoR I adaptor, digested
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 637.2; DB 7;
Pred. No. 5.7e-159;
1; Mismatches 4;
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701

360

300 641 821

540

480

761

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Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF116048 642 bp mRNA linear EST 24-OCT-2000 7n76g08.xl NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570638 3' similar to TR:Q9UMW4 Q9UMW4 DEATH EFFECTOR DOMAIN-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 ATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATCATTTA 881
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 642)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                    241 ccagriccaggicagaacagcagaaccagagcagcricggggrcagaggagcacagacaagg
                                                                                                                                                                                                                                301 GCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAGTCAATGATGAATCTTTCT
                                                                                                                                                                                                                                                                                                                                         762 GCCAGGATAATTTCTGCTTGCCATGGCCATCTGGCCACCAAGGAATTTCGCACCTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCTGACG
                                           181 TTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCCTCATCCACAGTGACCT
                                                                                                                                                                                                     GCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAGTCAATGAATCTTTCT
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/db_xref="taxon:9606"
/clone="lMAGE:3570618"
/tisave_type="fibrotheoma"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
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Seg primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTOR, ;, mRNA sequence.
BF116048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF116048.1 GI:10985524
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/dav stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/clone llb="Ull-E-EJ1"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; Ul-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                             University of lowa 1156 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 8250

Fax: 319 315 8250

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 626-650, >AT rich#Low_complexity (matched compliment)

Seq primer: M13 REVENSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes.
AGAATCAAGA; lens, CGATTAAGCA, eye anterior sequent,
AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Roveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI)."
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                     Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases I to 650)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="UI-E-EJ1-ajv-e-08-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCCTCCTAGTGAAGCAAACAGCATAC
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                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                    Contact: Soares, MB
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Matches 633
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     ORGANISM
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AI627241 621 bp mRNA linear EST 23-APR-1999 ty72all.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2284604 3' similar to TR:Q99710 Q99710 YY1-ASSOCIATED PACTOR 2. ;, mRNA
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                                                                                                              went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
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Pred. No. 9.9e-154;
1; Mismatches 5;
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98.9%;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AI627241.1 GI:4664041

ACCESSION VERSION KEYWORDS SOURCE

sapiens (human)

Homo

ORGANISM

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CSAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llhl.gov/bbrpt/image/fimage.html

Seq primer: -40UP from Gibco

High quality sequence stop: 463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NCIC CGAP Kidl1"
//clone lib="NCIC CGAP Kidl1"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NoT CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 132276-1323911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2284604"
/lab_host="DH10B"
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CK635466 The TB4 bp mRNA linear EST 28-JAN-2004 UI-M-HNO-cnl-o-13-0-UI.xl NIH_BMAP_HNO Mus musculus cDNA clone IMAGE:30643452 5', mRNA sequence.
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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
II (bases I to 744)
IIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                              61 CCAGTGTCACCAAGAAAACACCCAACAAAAAAAAAACCAAAGTCTGATATTCTGAAAG 120
                                                                                                                                                                                                                                                                      301 CCTCCACATCCTCTTCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGCA
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195 AGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAGACAAGGAAATTAGTC
                          375 CANATCACACCTCAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGTTGG
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// dev stage="10.5 dpc" |
// lab host="Hulbo (Ti phage resistant)" |
// lab host="Hulbo (Ti phage resistant)" |
// lab host="Hulbo (Ti phage resistant)" |
// lone="Organ: Head; Vector: pYX-Asc; Site I: EcoR I;
// lone="Organ: Head; Vector: pYX-Asc; Site I: EcoR I;
// lone="Organ: Head; Vector: pYX-Asc; Site I: EcoR I;
// lone="Organ: Head; Vector: pYX-Asc; Site I: EcoR I;
// lone |
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this CDNA
sequence: 708-733, -AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                 792 bp mRNA linear EST 29-APR-2004
UI-M-HOO-cpz-g-18-0-UI.rl NIH BMAP_HOO Mus musculus cDNA clone
CN533672
                                                                                                                       CACTTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATCATTTATAATTGGATGT 892
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 792)
                                                           82
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                                      TTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGA
                                                                                                                                                     64.1%; Score 607.2; DB 7; Length 792; 92.4%; Pred. No. 6.3e-151; ive 1; Mismatches 49; Indels 5.
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/mol_type="mRNA"
/strain="C57BL/6"
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/clone="IMAGE:30655169"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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Gaps

Best Local Similarity 92.4 Matches 671; Conservative

360

614

240

494 300 554

434

374

420 674 479 734 538 794 595 854

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AY400131 654 bp DNA linear GSS 15-DEC-2003
Homo sapiens RYBP gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                      TCTGCGATGTGAGGAAAGGCACCTCCACAGAAACCTCGGATCAATTCTCAGCTGGTGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 654)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Wite, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Tadd,W.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
GTATGAGATTCAAACCCTCCACCTGCCCATGCTTGCA-CCCTGGAGAGTCTTCTGTG
                                                                                                                                           84 TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG
                                                                                                   739 GACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCCTTGCCATGGGCATCTGGCCA
                                                                                                                                                                                                                                 CCAAGGAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTAT
                                                                                                                                                                                                                                                                                             596 CCAAGGAATTTCGTACCCTGACAGTTACTCTTGACACTTTTATGTATTCCATTGTTTTAT
                                                                                                                                                                                                                                                                                                                                                            859 ATGATTTTCCTAACAATCATTTATAAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.6%; Score 593; DB 9; L
ilarity 97.1%; Pred. No. 3.7e-147;
Conservative 1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="RYBP"
/locus_tag="HCM0455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .654
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="INMAGE:1064952"
/tissue_type="Upper Head"
/dev stage="9:5-10.5 dpc"
/lab host="Dhost Head"
/lab host="Dhost Head"
/lab host="Dhost Head"
/lab host="Dhost Head; Vector: pXX-Asc; Site 1: EcoR I;
/clone lib="NIH BMAP HN0"
/clone lib according lib according lip according li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAGTCAATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTACCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGTCACCAAGAAAACACCAACAAGAAAACAAAACCAAAGTCTGATATTCTGAAAGATCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTAGTGAAGCAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 TCACACCTCAAGGCCCCGGCTGAAAACGTGGACAGAGCACTGCACAGGAGTTGGCAGT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTGTGGGCAACGTCACGTCATTATCACAGACTTTAAGGAAAAGACTTCGCTCCTCATC 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATCCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGASCAGCTC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AGCAGTGAATGATGAATCTTTCTGAGATTGCACATGGAATTGTG-AAACTATGAATCAGG 479
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                                                                                                                                    This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 geagaagerceaaaagecercacaaaaaaaageceagagaaagacaagecarrragececag 60
      CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACACCTCAAGGCCCCGGCTGAAGAATGTGGACAGGAGCACCGCACAGCAGTTGGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                   The following repetitive elements were found in this cDNA gequence: 704_729, >AT_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.9%; Score 604.8; DB 7;
92.5%; Pred. No. 2.7e-150;
ive 1; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db xref="taxon:10090"
                                                                                                                                                                                                                                                           Seq primer: pXX-5.
Location/Qualifiers
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Best Local Similarity 92.5
Matches 668; Conservative
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                                                                                                    CCTCAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCAGCAGTTGGCAGTAACTG 443
                                                                                                                               TGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAGACTCGCTCCTCATCGACAT 503
                                                                                                                                                         CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGASCAGCTCGGGGT 563
                                                                                                                                                                                   CAGAGAGCACAGACAGGCTCCTCCCGTTCCTCCACGAGGGGGGGACATGTCAGCAG 623
                        CCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCCTCCTA 323
                                                          TCAATGATGAATCTTTCTGA 643
||||||||||||||||||
TCAATGATGAATCTTTCTGA 654
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Search completed: September 11, 2005, 15:26:44 Job time : 3620.35 secs

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September 11, 2005, 10:15:01; Search time 865.939 Seconds (without alignments) 8577.452 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

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5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

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6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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		Description		Sequence 569, App	Sequence 1792, Ap	Sequence 7027, Ap	Sequence 35, Appl	Sequence 121, App	Sequence 24859, A	Sequence 12, Appl
SUMMAKIES		CI.		6 21 US-10-505-680-569	US-10-956-157-1792	US-10-956-157-7027	US-10-489-740-35	US-10-103-313-121	US-09-918-995-24859	US-09-764-848-12
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	æ	Query Match	1 1 1 1 1	90.1	90.1	90.1	90.1	82.7	41.4	38.5
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Sequence 12, Appl Sequence 247, App Sequence 12, Appl	ñ.	570, 10941	Sequence 10941, A	Sequence 10204, A	Sequence 582, App	Sequence 1649, Ap	Sequence 22728, A	Sequence 4587, Ap						a	20, App					1510			26081,	26082,	26081,	2608		142,	142,	89,	89,
14 US-10-116-016-12 14 US-10-103-313-247 16 US-10-222-020-12	ם	21 US-10-505-680-570 17 US-10-242-535A-10941	18 US-10-085-783A-10941	-09-864-761-1020	₽		10 US-09-918-995-22728	21 US-10-956-15/-458/ 20 HS-10-357-930-54267			US-10		18 US-10-296-987-1	9 US-09-864-761-26844	US-10-877-320-20	5 US-10-029	S	US-10-363	US-10-363	21 US-10-363-483A-15102	US-10-029	o us	US-10-363	0 US-10-363	1 US-10-363-483A-26	7	15 US-10-279-964-29	US-10-314-669	ñ	4	14 US-10-105-891-89
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ALIGNMENTS

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90.1%; Score 1019.4; DB 21
Best Local Similarity 99.4%; Pred. No. 3.1e-292;
Matches 1023; Conservative 0; Mismatches 6;
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US-10-489-740-35

Sequence 35, Application US/10489740

Publication No. US20050112574A1

GENERAL INFORMATION:

APPLICANT: Bionomics Limited

TITLE NOF INVENTION: P9

FILE REFERENCE: Anglogenesis PCT

CURRENT APPLICATION NUMBER: US/10/489,740

CURRENT FILING DATE: 2004-03-15

NUMBER OF SEQ ID NOS: 216

SEQ ID NO 35
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ORGANISM: Homo sapiens
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: HUGAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE PALENTIN Version 3.2
SEQ ID NO 7027
LIENGTH: 1036
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Pred. No. 2.9e-292;
0; Mismatches 6; Indels 0;
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Best Local Similarity 99.4%;
Matches 1023; Conservative
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Sequence 121, Application US/10103313 Publication No. US20030082758A1 GENERAL INFORMATION:

RESULT 5 US-10-103-313-121

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant FILLE REPERENCE: PUZO7C1
CURRENT PAPLICAND NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 121
LENGTH: 2156 ö Score 935.8; DB 14 Pred. No. 3.6e-267; 0; Mismatches 7; Query Match 82.7%; Best Local Similarity 99.2%; Matches 951; Conservative TYPE: DNA CRGANISM: Homo sapiens US-10-103-313-121 721 925 781 g Š 셤

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cccceecreaaaacereegacaegacaecacaeacaegerrree 463
488 TGACGATTACTCTTG 502
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                                                                         1045 IGATITICCTAACAATCATITATAATIGGATGTGCTCCTGAATCTACTTTTATAAAA 1103
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Pred. No. 2.2e-128;
0; Mismatches 17; Indels 0;
                                                                                                                                                                    ; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
   APPLICANT: Hyeaq. Inc.
   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; TITLE OF INVENTION: ROW VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR PILING DATE: 1999-01-20
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PSESSEQ for Windows Version 3.0
; SEQ ID NO 24859
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24859
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Best Local Similarity 96.6%;
Matches 478; Conservative
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ORGANISM: Homo sapiens
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US-09-918-995-24859
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                                                                            APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT208
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 719
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Best Local Similarity 98.7%; Pred. No. 1.2e-118;
Matches 458; Conservative 2; Mismatches 2;
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US-09-764-848-12
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OTHER INFORMATION: n equals a,t,g, or NAMES STE
LOCATION: (626)
OTHER INFORMATION: n equals a,t,g, or NAMES/REY: SITTE
LOCATION: (643)
OTHER INFORMATION: n equals a,t,g, or OTHER INFORMATION: n equals a,t,g, or
; Sequence 12, Application US/09764848; Patent No. US20020077270A1; GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.5%; Score 436; DB 14; Length 719; Best Local Similarity 98.7%; Pred. No. 1.2e-118; Matches 458; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCGGCTGAAAAACGTGGGACAGGAGCACTGCACAGGCGTTTGG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCGGCTGAAAACGT-GGACAGGAGCACTGCACAGCAGTTGG 619
                                                                                                                  and Antibodies
                                                                                        TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
FILE REFERENCE: PT208C1
CURRENT APPLICATION VIMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: misc feature

LOCATION: (621)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (626)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (643)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (658)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (712)

COTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (712)

OTHER INFORMATION: n equals a,t,g, or c
                                  Sequence 12, Application US/10116016
Publication No. US20030054379A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
RESULT 8
US-10-116-016-12
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Sequence 247, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZOTCI
CURRENT APPLICANTON NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 98.7%; Pred. No. 1.2e-118;
Matches 458; Conservative 2; Mismatches 2;
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US-10-103-313-247
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                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (621)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (625)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (643)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (658)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (712)
                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                    SEQ ID NO 247
LENGTH: 719
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FILING DATE:
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                                  Sequence 12. Application US/10222020
Publication 10. Application US/10222020
Publication No. US200115739A1
GENERAL HIPORAMATION:
APPLICANT: RECENTED:
FILE REFERENCE: PTOGGE:
CURRENT PELLICATION NUMBER: US/10/22,020
PURENT PELLICATION NUMBER: US/10/21/36
PURENT PELLICATION NUMBER: US/21/36
PURENT PELLING DATE: 2000-09-21
PURENT PER PELLICATION NUMBER: US/21/36
PURENT PELLING DATE: 2000-09-31
PURENT PELLICATION NUMBER: US/21/36
PURENT PELLING DATE: 2000-09-31
PURENT PELLING DATE: 2000-09-31
PURENT PELLING DATE: 2000-09-31
PURENT PELLICATION NUMBER: US/21/36
PURENT PELLING DATE:
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APPLICATION NUMBER: 60/241,809
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APPLICATION NUMBER: 60/236,327
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APPLICATION NUMBER: 60/225,268
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                               US-10-222-020-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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R FILING DATE: 2000-10-13
R APPLICATION NUMBER: 60/239,937
R FILING DATE: 2000-10-13
R PRILICATION NUMBER: 60/241,787
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/246,474
                                                                                                                                                                                                                                        R FILING DATE: 2000-09-25
R RAPLICATION NUMBER: 60/229,343
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,345
R FILING DATE: 2000-09-01
R FILING DATE: 2000-09-01
R FILING DATE: 2000-09-01
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APPLICATION UNMBER: 60/225,759
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213
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FILING DATE: 2000-09-27
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FILING DATE: 2000-11-17
                                                                                      FILING DATE: 2000-12-08
APPLICATION WUMBER: 60/251,868
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/231,413
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/237,039
FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/237,038 FILING DATE: 2000-10-02
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FILING DATE: 2000-10-02
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FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/240,960
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FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,210
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
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                    APPLICATION NUMBER: 60/236,368
FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
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FILING DATE: 2000-10-02
                                                                     APPLICATION NUMBER: 60/251,856
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APPLICATION NUMBER: 60/234,997
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GARBALA INVOCATION APPLICANT: Penn, Sharron G.
APPLICANT: Fenn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRY
TOTHER REPEAT FILE APPLICANTON WIDNER: US/09/864,761
CURRENT FILEN DATE: 2000-03-04
REIOR FILENCATION WIDNER: US/09/664
REIOR FILENC DATE: 2000-03-04
REIOR FILENC DATE: 2000-01-04
REIOR FILENC DATE: 2001-01-30
REIOR PLILING DATE: 2001-01
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                                    AACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAATCACACCTCAAGG
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RILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Patent No. US20020048763A1
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Pred. No. 1.2e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               A APPLICATION NUMBER: 60/249, 211

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249, 215

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249, 264

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249, 214

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249, 297

OR APPLICATION NUMBER: 60/249, 297

OR APPLICATION NUMBER: 60/232, 400

OR FILING DATE: 2000-09-14

OR APPLICATION NUMBER: 60/232, 400

OR FILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/232, 081

OR APPLICATION NUMBER: 60/232, 081

OR APPLICATION NUMBER: 60/232, 080

OR FILING DATE: 2000-09-08

OR FILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/232, 080
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R APPLICATION NUMBER: 60/231,414
R FILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R FILING DATE: 2000-09-14
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R PELING DATE: 2000-09-14
R PELING DATE: 2000-09-14
R APPLICATION NUMBER: 60/232,397
R APPLICATION NUMBER: 60/232,397
R APPLICATION NUMBER: 60/249,208
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,213
R APPLICATION NUMBER: 60/249,212
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,212
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APPLICATION WUMBER: 60/232,401
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/241,808
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APPLICATION NUMBER: 60/241,786
FILING DATE: 2000-10-20
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,475
FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/249,245
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/241,826
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FILING DATE: 2000-11-17
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Best Local Similarity 98.7%;
Matches 458; Conservative ;
                                                                                                                                                                                                                                FILING DATE: 2000-11-17
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US-10-505-680-570/c

US-10-505-680-570/c

Sequence 570, Application US/10505680

Sequence 570, Application US/10505680

Sequence 570, Application US/10505680

Sequence 570, Application O. US2005005592A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America as represented by the APPLICANT: Jazaeri, Amir A.

APPLICANT: Jazaeri, Amir A.

APPLICANT: Jazaeri, Amir A.

APPLICANT: Liu, Edison T.

TITLE REFERENCE: LIU, Edison T.

TITLE REFERENCE: 4239-64452

CURRENT APPLICATION NUMBER: US/10/505,680

CURRENT FILING DATE: 2004-08-12

PRIOR PREJICATION NUMBER: 60/357,031

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 822

NUMBER OF SEQ ID NOS: 822
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                   Score 317.4; DB 21; Length 467;
Pred. No. 2.1e-89;
0; Mismatches 29; Indels 11;
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TGACATTTCTGAAGATCCTCCTAGTTGAAGCAAACAGCATACAG 467
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LOCATION: (1). [400)
OTHER INFORMATION: "n" represents an unknown nucleotide
                                                                                                         NAME/KEY: misc feature
; LOCATION: (1)...(467)
; OTHER INFORMATION: "n" represents an unknown nucleotide
US-10-505-680-571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1 SEQ ID NO 570
                                                                                                                                                                                                                          29.8%;
                                                                                                                                                                                                                                                                       Matches 424; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                          TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
                                                                                                                                                                                                                        Query Match
Best Local Similarity
SEQ ID NO 571
LENGTH: 467
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Publication No. US200509592A1

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

APPLICANT: The Government of the United States of America as represented by the APPLICANT: Jazaeri, Amir A.

APPLICANT: Jazaeri, Amir A.

APPLICANT: Boyd, Juff Boyd T.

APPLICANT: Liu, Edison T.

TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TP

FILE REFERENCE: 4239-64452

CURRENT APPLICATION NUMBER: US/10/505,680

CURRENT FILING DATE: 2004-08-12

PRIOR APPLICATION NUMBER: 60/357,031

PRIOR PRILING DATE: 2002-02-13
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 429;
                                                                               PEATURE:

OTHER INFORMATION: MAP TO AC012553.2

OTHER INFORMATION: EXPRESSED IN BOUNE MARROW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

US-09-864-761-4575
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                          Score 427.4; DB 9;
Pred. No. 3.2e-116;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.8%;
Best Local Similarity 99.8%;
Matches 428; Conservative
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                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-10-505-680-571
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US-10-085-783A-10941
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Sequence 10941, Application No. US20040013653A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILER REFERENCE: 4231/2005
CURRENT FFLING DATE: 2002-09-12
FRIOR PAPLICATION NUMBER: US 60/305,783
FRIOR PAPLICATION NUMBER: US 60/305,340
FRIOR PAPLICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2001-07-13
FRIOR PAPLICATION NUMBER: US 60/275,017
FRIOR PAPLICATION NUMBER: US 60/275,017
FRIOR FILING DATE: 2001-03-12
FRIOR FILING DATE: 2001-03-18
FRIOR FILING DATE: 2001-
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                                                                                                           Gaps
                                                                                                           10;
                                                     DB 21; Length 400;
                                                Query Match 28.0%; Score 316.6; DB 21; Length Best Local Similarity 93.5%; Pred. No. 3.1e-83; Matches 375; Conservative 0; Mismatches 16; Indels
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LOCATION: (29)...(29)

// OTHER INFORMATION: n is a,

US-10-242-535A-10941
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
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US-10-242-535A-10941
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US-10-505-680-570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
SOFTWARE: PARTICATION NUMBER: US 60/271,955
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PARTICIN VERSION 3.2
SOFTWARE: PARTICIN VERSION 3.2
                                                                                                               234 CTTCAGAAACAGTGCTGAAGCCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTC
                                                                                                                                                                                                    294 CACCAGAAAACCTCGGATCAATTCTCAGCTGGCACAACAACAAGTGGCACAAACAGTATGC
                                                                                                                                                                                                                                                                                               155 CACCAGAAAACCTCGGATCAATTCTCAGCTGGTGGCACAAGAAGTGGCACAACAGTATGC
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                                                                                           174 GCCAAAAAGACAAGCGAAACCTGCCGCAGACGAAGGGTTTTTGGGATTGTAGCGTCTGCAC
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                                               Gaps
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    DB 17; Length 326;
                                               4; Indels
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Pred. No. 4.6e-74;
0; Mismatches 4;
Score 285.6; DB 17
Pred. No. 4.6e-74;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10941, Application US/10085783A; Publication No. US20040037841A1; GENERAL INFORMATION:
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LOCATION: (29)
CTHER INFORMATION: n is a, c,
US-10-085-7838-10941
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Best Local Similarity 98.6%;
Matches 288; Conservative (
    25.3%;
98.6%;
  Query Match
Best Local Similarity 98.6<sup>5</sup>
Matches 288; Conservative
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OTHER INFORMATION: n is
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LOCATION: (8)...(8)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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AX138319 Sequence
AX092139 Sequence
AX138319 Sequence
AX13819 Homo sapi
BC014959 Homo sapi
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AX821956 Homo sapi
AR029551 Homo sapi
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BC053016 Mus muscu
BC063016 Mus muscu
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                           4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                    nucleic search, using sw model
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ALIGNMENTS

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CUS	AX092138 DNA	linear PAT 21-MAR-2001	н
FINITION	8 from Patent WO		
RSION	AX092138.1 GI:13444365		
YWORDS			
URCE	Homo sapiens (human)		
ORGANISM			
	Eukaryota, Metazoa, Chordata, Craniata, V Mammalia, Eutheria, Primates, Catarrhini,	Craniata; Vertebrata; Euteleostomi; Catarrhini: Hominidae; Homo.	
TODOGO	, , , , , , , , , , , , , , , , , , , ,		
AUTHORS	Noteborn, M.H. and danen-van Oorschot, A.A.		
TITLE	Apoptin-associating protein		
JOURNAL	Patent: WO 0116165-A 8 08-MAR-2001;		
	Leadd B.V. (NL)		
ATURES	Location/Qualifiers		
source	1947		
	/organism="Homo sapiens" /mol type="unassigned DNA"		
	/db xref="taxon:9606"		
misc_feature	eature 1947 /note="'AAP-1-a nucleic acid wherein N "" "	rein N can be A, C, G or	
IGIN	•		
Query Match	99.78; S	Length 947;	
Best Loca. Matches S	Best Local Similarity 100.0%; Fred. No. 1.4e-255; Matches 947; Conservative 0; Mismatches 0;	Indels 0; Gaps	· 0
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		AGGCCACGAAGGCCGAAACAG 60	
	61 TGCTGAAGCCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACC	AGGCACCTCCACCAGAAACC 120	
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/wol_type="unassigned DNA"
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Patent: EP 1108785-A 4 20-JUN-2001;
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/note="Apoptin-associating protein"
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Patent: EP 1081226-A 4 07-MAR-2001;
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/organism="Homo sapiens"
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Sequence 4 from Patent EP1081226.
AX138324
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Mammalia; Butheria; Primates;
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Sequence 8 from Patent EP1083224.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Patent: WO 0116165-A 9 08-MAR-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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989 GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGTAT
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                                            804 GAATTICGCACCCIGACGATTACICITGACACTITITATGTATICCATIGITITATATATGAT
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="texon:9606"
/note="Description of Combined DNA/RNA Molecule:
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Patent: EP 1081226-A 12 07-MAR-2001;
Leadd B.V. (NL)
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                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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93.2%; Score 883; DB 6; Length 1131;
Best Local Similarity 97.7%; Pred. No. 1e-217;
Matches 903; Conservative 2; Mismatches 18; Indels
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                                                                                                                                                                                                                                                  /note="'AAP-1-b nucleic acid'"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .1131
                                                                                                                     Apoptin-associating protein
Patent: EP 1083224-A 9 14-MAR-2001;
Leadd B.V. (NL)
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        GI:14274285
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Homo sapiens (human)
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2344 bp mRNA linear PRI 29-JUN-2004 Homo sapiens RING1 and YY1 binding protein, mRNA (cDNA clone MGC:33492 IMAGE:4813939), complete cds. BC036459 GI:22209025
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATGTAT
                                                                                                                                                                                                                                                                                                                                            GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT
  CCTCAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTG
                                                                                                                                                                      TCAATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATG
                                                                                                                                                                                                                        AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGACAT
                                                                                                                                                                                                                                   GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA
                                                                          CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGASCAGCTCGGGGT
                                                                                                                         CAGAGAGCACAGACAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                   TTTCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="'AAP-1-b nucleic acid'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA

    1131
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Patent: EP 1108785-A 5 20-JUN-2001;
Leadd B.V. (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX114152
Sequence 5 from Patent EP1108785.
AX114152
AX114152.1 GI:14031160
                                                                                                                                                                                                                                                                                                                                                                                                                              TTYGTGGCCTCGAGAGATCTATGA 947
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Best Local S:
Matches 902
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX114152
LOCUS
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GCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACACTTTA 1072
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                                                                                                                  1 ACCANACCCAAAAAAAAGAGATCTGGAATTCGGATCCTCGAGGCCACGAAAGAG
                                                                                                                                                      233 AgcgaAaccrgccacadaacgAaagcgrrrrrgcgarrgragcgrcrcgcaccrrcagAAAcAG
                                                                                                                                                                                                                                                                                                                                                CCCTABABAGGAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AAAGACCAGCGAAACAAATCACACCTCAAGGCCCCGGCTGAAAAACGTGGACAGGAGCAC
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                                        Length 2344;
                                                                              Indels
                                      Score 871.2; DB 9;
Pred. No. 1.2e-214;
1; Mismatches 31;
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96.5%;
                                                                                888; Conservative
                                            Query Match
Best Local Similarity
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CQ715417
                                                                                  Matches
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bornaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madoriques, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jonee, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 46 Row: e Column: 4. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTWGDKKSPTRPKRQAKPATDEGFWDCSVCTFRNSAEAFKCSIC
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VTVGRVTVIIITDPKEKTRSSSTSSSTVTSSAGSEQQNQSSGGSESTDKGSSRSSTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (09-AUG-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tisaue Procurement: Miklos Palkovits, M.D., Ph.D.
Tisaue Procurement: Miklos Palkovits, M.D., Ph.D.
Tisaue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadm@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="RING1 and YY1 binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:33492 IMAGE:4813939"
/tissue type="Brain, hippocampus"
/clone lib="NIH MGC_95"
/lab_host="DH10B"
/note="Wector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAH36459.1"
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/db_xref="LocusID:23429"
/db_xref="MIM:607535"
1895_.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="MIM:607535"
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/gene="RYBP"
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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COMMENT
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540

772

712

900 832 9 892

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/translation="MODKKSPTRPKRQAKPAADEGFWDCSVCTFRNSAEAFKCSICDV
KRGTSTRKPRINGQLVAQQVAQYATPPPPKKEKKEKVBKQDKEKPECDKEISPSVTK
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VGNVTVIITDFKEKTRSSSTSSSTVTSSAGSEQQNQSSSGSESTDKGSSRSSTPKGDM
SAVNDESF"
                                                                                                                                                                                                                                                                                              PRI 12-MAY-2004
mRNA, complete
                                     803
                                                                                                         863
       761
                                                                       821
                                                                                                                                         881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral apoptosis agonist Apoptin and exerts tumor-preferential cell
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danen-van Oorschot, A.A.A.M., Voskamp, P., Seelen, M.C., van Miltenburg, M.H., Bolk, M.W., Tait, S.W., Boesen-de Cock, J.G., Rohn, J.L., Borst, J. and Noteborn, M.H.

Human death effector domain-associated factor interacts with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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                                                                                                                                                                          920
                                                                                                                                                                                                          938
                                                        702 AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCTTGGAGAATCTTCTGTGGACAT
                                       744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACAAG
                                                                                                         804 GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT
                                                                                                                            822 GAATTICGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1021)
Danen-van Oorschot, A.A.A.M., Boesen-de Cock, J.G.R., Borst, J.
                                                                                                                                                                                            882 TITCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAAAA
                                                                                                                                                                         864 TITCCTAACAATCAITIATAAATTGGATGTGCTCCTGAATCTACTITITATAAAAAAA
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Danen-van Oorschot, A.A.A.M., Boesen-de Cock, J.G.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                                                                              AY228125 1021 bp mRNA linear Homo sapiens apoptin-associating protein 1 (AAP1)
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/protein_id="AAO73587.1"
/db_xref="GI:29423711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noteborn, M.H.M.

AAP-1, a binding partner of Apoptin, induces tumor cells but not in normal diploid cells Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 870; DB 9; 1
Pred. No. 2.3e-214;
1; Mismatches 17;
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/db_xref="taxon:9606"
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Submitted (31-JAN-2003) Leadd
AL, The Netherlands
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AY228125.1 GI:29423710
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Best Local Similarity 98.0%;
Matches 879; Conservative
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                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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       PAT
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Patent: WO 02068579-A 1351 06-SEP-2002;
PE Corporation (NY) (US)
       DNA
Sequence 1351 from Patent W002068579.
CQ715417
                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                    91.9%; Score 870; 98.0%; Pred. No. 2
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Location/Qualifiers
                                                     CQ715417.1 GI:42276274
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Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

ORGANISM

BC014959.1 GI:15928992

BC014959

ACCESSION

VERSION KEYWORDS SOURCE

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Strausberg, E. Feingold, B. A., Grouse, L. H., Derge, J. G.,
Rausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. P., Zeeberg, B., Buetow, K. H., Scheefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. B., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. M.,
Villalon, D. K., Muzny, D. M., Sodergren, B. J., Lu, X., Gibbs, R. A.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Butterfield, Y. S., Krzywinski, M. I., Stallaka, U., Sanius, D. E.,
Schnerch, A., Schein, J. E., Jonnes, S. J. and Marra, M. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL plate: 34 Row: o Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24432049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Samilus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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/gene="RYB"
/codon start=1
/product="RING1 and YY1 binding protein"
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/mol_type="mRNA"
/db xrefa"taxon:9606"
/clone=mGC:23015 IMAGE:4902201"
/tissue_type="Muscle", rhabdomyosarcoma"
/clone_lib="NIH MGC_17"
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Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procuremant: ArCc
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PAT 17-JUL-2003
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Gerstin, E.H., Patterson, C., Baughn, M.R., Azimzai, Y. and Lu, D.A.M.
Human transcriptional regulator molecules
Patent: JP 2002513554-A 43 14-MAY-2002;
INCYTE PHARMACEUTICALS INC
S. Homo sapiens (human)
PN JP 2002513554-A/43
PD 14-MAY-2002
                                                                                                                                                                                                            Euteleostomi;
1115
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Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1
1 (bases 1 to 3641)
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60/102745
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Incyte clone 3149729CB1
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                                                                                   3641 bp
Human transcriptional regulator
BD209971
                                                                                                                                                                                                                                                                                                                                                 OS Homo sapiens (human)
P 2002513554-A/43
PD 14-MAY-2002
PF 04-MAY-1999 JP 2000547113
PR 05-MAY-1999 US 60/084254
02-OCT-1998 US 60/102745
PI JENNIFER L HILLIMAN, OLGA BAN
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/organism="Homo
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Homo sapiens (human)
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                                                                    /trānslation="MTWGDKKSPTRPKRQAKPAADEGFWDCSVCTFRNSAEAFKCSIC
TWKKGTSTRKPRINSQLVAQQYAJPPPFKKEKKBKVROQDKEKPBKDKBISPSV
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VTVGNVTVIITDFKEKTRSSSTSSTYTSSAGGEQQNOSSSGBESTDKGSSRSSTPKG
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1; Mismatches 17;
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/db_xref="GI:15928993"
/db_xref="LocusID:23429"
/db_xref="MIM:607535"
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I (bases I to 1036)

Zheng,L., Schickling,O., Peter M.E. and Lenardo,M.J.

The death effector domain-associated factor plays distinct regulatory roles in the nucleus and cytoplasm

J. Blol. Chem. 276 (34), 31945-31952 (2001)

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Method to modify differentiation of pluripotential stem
Patent: WO 03068961-A 84 21-AUG-2003;
Axordia Limited (GB)
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|mol_type="unassigned DNA"
|db_xref="taxon:9606"
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AX821956
AX821956.1 GI:39725177
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VDWKGTSTRKRRINSQLYAQQVAQQVATPPPRKEKKEKKEKVEKQDKEKPEEUKBISBSV
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TKKATNKKTRFRSDILLAPPSEANSIQSANATIKTSETNHTSRPRLKAVDRSTAQQLA
VTVGNVTVIITDFKEKTRSSSTSSTTTSSAGSEQQNQSSGSBSTDKGSSRSSTPKG
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/protein id="AAD51858.1"
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/mol_type="mRNA"
/cell_type="mitogen activated peripheral blood
lymphocytes"
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1; Mismatches 18; Indels 0;
2 (bases 1 to 1036)
Zheng, L.X., Yoo, T. and Lenardo, M.J.
A novel protein associated with Caspase-10 DED domain
Unpublished
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/note="YAF2 homolog; DEDAF; RYBP"
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ALIGNMENTS

Nucleotide sequence of apoptin-associating protein 1 cDNA clone a. Apoptin-associating protein; AAP; apoptosis; cell proliferation; cell death; autoimmune disease; cancer; ss. New nucleic acids encoding apoptin-associating proteins useful inducing apoptosis, particularly p53 independent apoptosis, or treating cancers or autoimmune diseases. Noteborn MHM, Danen-Van Oorschot AAAM; AAF55595 standard; cDNA; 947 BP 01-SEP-2000; 2000WO-NL000612. 99EP-00202858 99EP-00203465 (first entry) WPI; 2001-235090/24 (LEAD-) LEADD BV. WO200116165-A2. 02-SEP-1999; 21-OCT-1999; Homo sapiens 29-MAY-2001 08-MAR-2001 AAP55595; RESULT 1 AAF55595

Claim 6; Fig 1; 50pp; English.

for for

in cancer The present sequence encodes a human apoptin-associating protein 1 (AAP1). The protein is capable of providing apoptosis. AAP polypeptides and polymucleotides are useful for inducing apoptosis, particularly when apoptosis is p53-independent. They may be used to produce pharmaceutical compositions which are used for treating a disease where enhanced cell proliferation or decreased cell death is observed, particularly in cancer or in autoimmune diseases, for diagnosing a disease related with

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aberrancies in the apoptotic process, and for detecting the presence cancer cells or cells that are prone to cancer
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                                                                                                           Length 947;
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                                                               Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;
                                                                                                                                                          Indels
                                                                                                              Score 944.2; DB 4;
Pred. No. 7.9e-250;
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The present sequence encodes an apoptin-associating proteinaceous substance (apoptin-associating protein 1 (AAP-1), which is capable of inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for inducing a p51-independent apoptosis. They are used for treating a disease where enhanced proliferation or decreased cell death is observed e.g. cancer or autoimmune disease. They are also used for diagnosis of diseases related with aberrations in the apoptotic process such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
transl except= (pos: 144. .146, aa: Xaa)
note= "Xaa is an unspecified residue; encodes AAB67553"
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/note= "Xaa is an unspecified residue; encodes AAB67557"
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                                                                                                                                                                                                proteinaceous substance; cell proliferation;
protein 1; AAP-1; apoptosis; cell death; cancer;
88.
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P-PSDB; AAB67552, AAB67553, AAB67554, AAB67555, AAB67556, AAB67557,
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                                                                                                                                                                        Nucleotide sequence of an apoptin-associating protein.
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'note= "encodes AAB67554"
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/note= "encodes AAB67558"
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AAF55404 standard; DNA; 947
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                                                                                                                                                                                                                                 Apoptin-associating apoptin-associating autoimmune disease;
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protein; AAP; apoptosis; p53; cell proliferation; autoimmune disease; cytostatic; immunosuppressive;

Apoptin-associating protei cell death; cancer; autoim gene therapy; AAP-1-a; ss.

sapiens EP1083224-A2

Ношо

Danen-Van Oorschot AAAM;

WPI; 2001-228257/24.

99EP-00202858.

01-SEP-2000; 02-SEP-1999; 21-OCT-1999;

14-MAR-2001

(LEAD-) LEADD BV. Noteborn MHM,

Apoptin-associating protein (AAP)-1-a nucleotide sequence

29-MAY-2001

AAF57184;

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                    Indels
Query Match 99.7%; Score 944.2; DB 4; Best Local Similarity 100.0%; Pred. No. 7.9e-250; Matches 947; Conservative 0; Mismatches 0;
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The invention provides isolated or recombinant nucleic acid (I), its functional encoding an apoptin-associating proteinaceous (AAP) substance capable of apoptosis. (I), the vector comprising (I), the host cell comprising the vector and the proteinaceous substance encoded by (I) are useful for inducing apoptosis, particularly p53-independent apoptosis, and for treating a disease where enhanced cell proliferation or decreased cell fath is observed, such as cancer or an autoimmune disease. A composition comprising the nucleic acid or the AAP may further be used for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells or cells that are process. The present sequence represents the nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.7%; Score 944.2; Best Local Similarity 100.0%; Pred. No. 7.9 Matches 947; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer or autoimmune disease.
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The present sequence encodes a human apoptin-associating protein 1 (AAPI). The protein is capable of providing apoptosis. AAP polypeptides and polymucleotides are useful for inducing apoptosis, particularly when apoptosis is p53-independent. They may be used to produce pharmaceutical compositions which are used for treating a disease where enhanced cell proliferation or decreased cell deach is observed, particularly in cancer or in autoimmune diseases, for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells or cells that are prone to cancer
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                             New nucleic acids encoding apoptin-associating proteins useful inducing apoptosis, particularly p53 independent apoptosis, or treating cancers or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                      Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local Similarity 97.7%; Pred. No. 6.7e-233;
Matches 903; Conservative 2; Mismatches 18;
                                                                                                  Claim 6; Fig 2; 50pp; English.
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                                                                                           AAAGACCAGCGAAACAAATCACACCTCAAGGCCCCGGCTGAAAAAGGTGGACAGGAGCAC
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21-OCT-1999;
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                                                                 Length 1131;
                                           Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
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Pred. No. 6.7e-233;
2; Mismatches 18;
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                                                                 Query Match 93.2%;
Best Local Similarity 97.7%;
Matches 903; Conservative
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                                                                                           The present sequence encodes an apoptin-associating proteinaceous substance (apoptin-associating protein 1 (AAP-1), which is capable of inducing apoptosis. AAP-1 polypeptides and polynucleotides are useful for inducing a p53-independent apoptosis. They are used for treating a disease where enhanced proliferation or decreased cell death is observed
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 GAATTTCGCACCCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT
                                    GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTAFTCCATTGTTTTATATGAT
                                                                                TTTCCTAACAATCATTTATAAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAAAGCC
                                                                                                                                                                                                                                                                                          Apoptin-associating proteinaceous substance; cell proliferation; apoptin-associating protein 1; AAP-1; apoptosis; cell death; cancer; autoimmune disease; ss.
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P-PSDB; AAB67559, AAB67560, AAB67561, AAB67562, AAB67563.
                                                                                                                                                                                                                                                                              Nucleotide sequence of an apoptin-associating protein.
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/note= "encodes AAB67560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides isolated or recombinant nucleic acid (1), its functional encoding an apoptin-associating proteinaceous (AAP) substance capable of apoptosis. (1), the vector comprising (1), the host cell comprising the vector and the proteinaceous substance encoded by (I) are useful for inducing apoptosis, particularly p53-independent apoptosis, and for treating a disease where enhanced cell proliferation or decreased cell death is observed, such as cancer or an autoimmune disease. A composition comprising the nucleic acid or the AAP may further be used for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells that are prone to cancer. The present sequence represents the nucleotide sequence of the AAP-1-b protein
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                                                                                                                                                                                                                                          Apoptin-associating protein, AAP, apoptosis; p53; cell proliferation, cell death, cancer; autoimmune disease; cytostatic; immunosuppressive; gene therapy; AAP-1-b; ss.
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/transl_except= (pos:937. .939, aa:Xaa)
/transl_except= (pos:940. .942, aa:Xaa)
/transl_except= (pos:1015. .1017, aa:Xaa)
/transl_except= (pos:1015. .1017, aa:Xaa)
/transl_except= (pos:1045. .1047, aa:Xaa)
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                                                                                                                                                                                          Apoptin-associating protein (AAP)-1-b nucleotide sequence
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                              AAF57185 standard; cDNA; 1131
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P-PSDB; AAB62059.
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CCAAGAAAATACCAAGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCCTCCTA
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                                                                                        269 TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG
                                                                                                                        CNCAACAAGAGGCACAGGTATGCCACCCCCACCCCCTAAAAAGGAGAAGAAGAGGAGA
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                                                       84 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAACCTCGGATCAATTCTCAGCTGGTGG
                                                                                                                                             CCTCAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTG
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Best Loca Matches

383 578 443 638 503 698 563 758 623

458 323

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HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; ss; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
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                                399 AAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAAAGACAAGGAAATTAGTCCTAGTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the isolation of novel genes (ACF34446-ACF34559) encoding proteins (ABR64180-ABR64281) involved in the process of angiogenesis. The nucleic acid molecules are useful in identifying and/or obtaining full-length human eness involved in an angiogenic process. The nucleic acid molecule, polypeptides or complexes encoded, cells or genetically modified non-human animals derived from these are useful for the screening of candidate pharmaceutical compounds used in treating angiogenesis related disorders. They are also useful for diagnosing, prognosticating or treating an angiogenesis or is a disorder in which a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis, involves uncontrolled or enhanced angiogenesis or is a disorder in which a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or cardiovascular diseases such as atherosclerosis), or involves inappropriately arrested or decreased angiogenesis or is a disorder in which an expanding vasculature is of benefit (e.g. ischemic limb disease or coronary artest disease). The mucleic acid sequence is useful for manufacturing a medicament for the nucleic acid sequence is related disorder. This sequence corresponds
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  ophthalmological;
                   antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis; gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; schemic limb disease; coronary artery disease; gene; ds.
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    antidiabetic;
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98.0%; Pred. No. 2.6e-229;
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    Cytostatic, antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claim 2; SEQ ID NO 35; 90pp; English.
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; 2001AU-00008210.
; 2001AU-00008532.
; 2001AU-00008838.
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11-CCT-2001; 2001AU-000085210.
29-CCT-2001; 2001AU-00008532.
13-NOV-2001; 2001AU-00008838.
28-AUG-2002; 2002AU-00951032.
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Matches 879; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; inhibitory RNA; RNAi; Notch signaling target gene; phenotype;
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                                                                                                                                                                                                CCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGASCAGCTCGGGGT
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13-FEB-2002; 2002GB-00003387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-697528/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ52410-Z52474 are human transcriptional regulator molecule (HTRM)
                                                                                                                                                                                                                                                                                         New peptides useful for diagnosis, prevention and treatment of immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3641 BP; 1081 A; 718 C; 738 G; 1104 T; 0 U; 0 Other;
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                                                                                                                                                  I, Reddy R,
Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.9%; Score 870; DB 3; I
98.0%; Pred. No. 4.5e-229;
iive 1; Mismatches 17;
                                                                                                                                                il P, Yue H,
Baughn MR, A
                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 176-177; 193pp; English
                                                                                                                                                  Lal P,
98US-0084254P.
98US-0095827P.
98US-0102745P.
                                                                                                                                                  Bandman O, L
Patterson C,
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                                                                                                  (INCY-) INCYTE PHARM INC.
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02-OCT-1998;
                                                                                                                                                Hillman JL,
Gerstin EH,
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The invention relates to an inhibitory RNA (RNAi) molecule derived from a nucleic acid molecule comprising a defined nucleic acid sequences given in the specification or a sequence which hybridizes to the sequences and encodes a Notch signaling target gene or which is a degenerate as a result of the genetic code of the sequences. The methods and compositions of the present invention are useful for manipularing the phenotype of stem cells, preferably pluripotent stem cells. This sequence corresponds to one of the nucleic acid molecules of the invention.
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                                                                                                                                                                                                                                                                                                   TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG 143
                                                                                                                                                                                                                                                                                                                        TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG 254
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                                                                                                                                                                                                                                       GGAATTCGGATCCTCGAGGCCACGAAGGCCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA
                                                                                                                                                                                                          Gaps
                                                                                                                                                                      Score 868.4; DB 10; Length 1036;
Pred. No. 6.8e-229;
1; Mismatches 18; Indels 0;
                                                                                                                                          Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other;
                                                                                                                                                                       91.7%;
97.9%;
                                                                                                                                                                                                          Matches 878; Conservative
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The invention relates to a method of classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a pattern of expression in the ovarian tumor of several markers given in the specification; and (2) comparing a similarity of the pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. The method is useful for classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. This sequence corresponds to an ovarian cancer -related gene having an altered pattern of expression in ovarian cancer. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from WIPO at ö Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of several markers. 194 143 254 203 314 aagttgaaaagcagcacaaagagaacctgagaaagacaaggaaattagtcctagtgt 263 83 975 TTTCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTAATAAAAA 1031 Ovarian cancer-related DNA #554 with altered ovarian cancer expression. CNCAACAAGTGGCACAACAGTATGCCACCCCACCCCCTAAAAAGGAGAAGAAGAAGA GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA 135 GGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGCTGAAGCCTTTAAATGCAGCA TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG Gaps BRCA-1-like; BRCA-2-like; non-BRCA-like; ö DB 10; Length 1036; Sequence 1036 BP; 327 A; 265 C; 234 G; 210 T; 0 U; 0 Other; 18; Indels Score 868.4; DB 10 Pred. No. 6.8e-229; 1; Mismatches 18; Disclosure; SEQ ID NO 569; 137pp; English. ftp.wipo.int/pub/published_pct_sequences) (USSH) US DEPT HEALTH & HUMAN SERVICES. (SLOK) SLOAN KETTERING INST CANCER RES. 1; gene expression; primer; cancer 13-FEB-2002; 2002US-0357031P. Liu ET; 91.7%; 97.9%; ADK61399 standard; DNA; 1036 13-FEB-2003; 2003WO-US004688 Best Local Similarity 97.9 Matches 878; Conservative ovarian tumor; Jazaeri AA, Boyd J, WPI; 2003-689589/65 WO2003068054-A2. Ното варіелв 06-MAY-2004 21-AUG-2003 ADK61399; 24 84 195 144 255 204 Query Match MON 1399

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This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention way be useful for gene therapy. The invention way be useful for diagnosing or treating a hypoxia-regulated condition, such as tumourigenesis, anglogenesis, apoptosis, inflammation, erythropoisess or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion inflammatory conditions or wound healing. The present sequence is that of a disease related protein encoding DNA sequence of the invention.
                                                                                                                                                                                                                                                                             New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.
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Local Similarity 97.8%; Pred. No. 3.9e-228;
les 877; Conservative 1; Mismatches 19;
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23-AUG-2001; 2001GB-00020558. 05-OCT-2001; 2001GB-00024037.
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2000US-023944P.
2000US-023144P.
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CCTCATCCACAGTGACCTCCAGTGCAGGTCCGAACAGCAGAACCAGAGCAGCTCGGGGT 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding novel human neoplastic disease associated polypeptide #111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; neoplastic disease associated polypeptide; cancer; gene therapy; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
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                                                                                                               TCAATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATG
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02-MAR-2000; 2000US-0184664P.
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16-MAR-2000; 2000US-0189374P.
19-MAY-2000; 2000US-0199173P.
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2000US-0225213P.
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Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;

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Claim 4; SEQ ID NO 121; 687pp; English
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                                                                   2000US-0246528P

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P-PSDB; AAU21678.
006-NOV-2000;
08-NOV-2000;
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Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukasemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocycoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders under alsorders, immune system disorders, muscullar disorders cardiovascular disorders, astrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for the novel human neoplastic disease associated polypeptides of the the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences

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                                           24 GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA
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Query Match 90.7%; Score 859; DB 4; L
Best Local Similarity 97.9%; Pred. No. 3.8e-226;
Matches 879; Conservative 1; Mismatches 17;
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ADC46035 standard; cDNA; 2156 ADC46035; RESULT 13
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Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; rethematoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury; anflammatory bowel disease; crobm's disease; neurodegenerative disorder; Alzhelmer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; AIDS; cachexia; anorexia; wound healing; epithelial cell proliferation; Human; ss.
                                         Human neoplastic disease-associated gene 111 cDNA #1
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304 ACCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCTGAAAGATCCTCCT 363
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                                         323 AGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAATCAC
                                                               383 ACCICAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACT
                                                                                                                                                 GTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACA
                                                                                                                                                                                                                                                                                                                         544 TCCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGCAGCTCGGGG
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STACHE-CRAIN E
DICKSON M C.
JONES L W.
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(DICK/)
(JONE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to one of 238 disclosed human neoplastic disease-
associated polypeptides encoded by 171 disclosed CDNA sequences
(including their domains, epitopes, full-length proteins, allelic variants
or species homologues). Also included are there encoding nucleic acids, a
recombinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
antibody that binds specifically to the local and partering,
treating or ameliorating a medical condition, diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject,
identifying a binding partner to the polypeptide, identifying an activity
in a biological assay, and the gene corresponding to the CDNA sequence.
The polypeptides, polynucleotides and antibodies are useful for
aneliorating preventing, diagnosing, prognosticating, treating or
aneliorating medical conditions such as hyperproliferative diseases or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
canaemia or thrombocytopaenia), elegic reactions including asthma or
cecema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCGATGTGAGGAAAGGCACCTCCACCA-GAAAACCTCGGATCAATTCTCAGCTGGTG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAAGACAAGGAAATTAGTCCTAGTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated human neoplastic disease-associated polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2156;
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Pred. No. 3.8e-226;
1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 121; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     SC;
                                      01-DEC-2000; 2000US-0250160P.

01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-0251030P.

05-DEC-2000; 2000US-0251030P.

05-DEC-2000; 2000US-025104P.

06-DEC-2000; 2000US-025104P.

08-DEC-2000; 2000US-0251060P.

08-DEC-2000; 2000US-0251060P.

08-DEC-2000; 2000US-0251060P.

08-DEC-2000; 2000US-0251060P.
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Best Local Similarity 97.9%;
Matches 879; Conservative
                                                                                                                                                                                                                                                                                      2001US-0259678P
                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                          2003-786918/74
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      17-NOV-2000;
17-NOV-2000;
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AAI14743 standard; DNA; 429

12-OCT-2001

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
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                                                 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.6%; Score 469.6; DB 9; Length 502; 96.6%; Pred. No. 5.4e-119; tive 1; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 502 BP; 138 A; 140 C; 118 G; 105 T; 0 U; 1 Other;
                                                                                                                                                       Claim 1; SEQ ID NO 24859; 44pp; English
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                                                                                                                antisense DNA or RNA
                WPI; 2003-615964/58
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RESULT 15 AAI14743/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                           Probe #4676 for gene expression analysis in human cervical cell sample.
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                                                                                                     human; microarray; gene expression; cervical epithelial cell;
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                      Homo sapiens.
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26-MAY-2000;
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Db 189 TGAAATTGCACATGGAATTGTGAAACTATGAATCAAGGGTATGAAATTCAAAACCTCCAC 130

Qy 701 CTGCCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGACATCGAACTCTAGTGATGT 760

Db 129 CTGCCCATGCTGCTTGCCATGGGAAATCTTCTGTGGACATCGACCTCTTAGTGATGC 70

Qy 761 TGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCACCTCTTAGTGATGC 70

Db 69 TGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCTTGAC

Qy 821 GATTACTT 829

Db 9 GATTACTT 1
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Search completed: September 11, 2005, 10:36:34 Job time : 589.596 secs

113,427, A 111, Appl 20, Appl 00, Appl 0, Appl 1, Appl Appl Appl

Sequence Sequence Sequence

Sequence 11, A Sequence 20, A Sequence 20, A Sequence 20, A Sequence 20, A Sequence 24, A Sequence 8, Ap Sequence 13042 Sequence 12096 Sequence 16097 Sequence 16097 Sequence 16097 Sequence 19, A Sequence 11114

Title: Perfect score:

Sequence:

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Scoring table:

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147 AACAAGTGGCACAACAGTATGCCACCCCACCACCCCTAAAAAGGAGAAGAAGAAAAG
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TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961

PILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm
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Best Local Similarity 61.7%; Pred. No. 3.4e-19;
Matches 148; Conservative 0; Mismatches 92;
                   US-10-081-563-25
US-10-027-983-11
US-10-027-983-11
US-09-012-515A-20
US-09-012-515A-20
US-09-012-504A-20
US-09-012-594A-20
US-09-012-594A-20
US-08-408-095-24
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; OTHER INFORMATION: Xaa=Lys or Thr
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OTHER INFORMATION: m=a 03
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-318-947A-1
US-08-318-947A-1
US-09-269-617-13
US-09-621-976-2061
US-09-902-540-1318
US-09-902-540-1318
US-08-902-540-1318
US-09-902-540-1357
US-09-902-540-1357
US-08-467-96A-11247
US-08-467-968-115-29
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3-08-467-963C-28
3-08-838-189D-28
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Score

Result

40.6

40.6 40.6

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92; Indels

Length 376;

us-09-655-109a-4.rni

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53 ACCAAACCCAAAAAAAAAAAAATCTGGAATCCTCGAGGCCACGAAGGCCGGAAATC 112
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APPLICANT: Anderson, Paul J.
APPLICANT: Tian, Qingsheng
TITLE OF INVENTION: T1A-1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSPONDENCE ADDRESS:
ADDRESSPONDENCE SUGITURE, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
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COMPUTER: IBM PC compatible
COMPATRING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/269,617
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09269617
Patent No. 6204253
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FACTORS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08318947A Patent No. 5798245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA library
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1075 RRRRRRRRATCGCA 1061
                                                                                                                                                                                                                                                                              369 GCGAAACAAATCACA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
CELL TYPE: B-lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 88.1;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 TGAAGCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE -
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-269-617-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-269-617-11
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                                                           313 TAGAAAAAGAAAAAGTGAAAAGGAAACAACTAGCAAAAAGATAGCCATAAGAMAACCA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 AGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGGAAAACCTGAGAAAGACAAGGAAA 248
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RESULT 2
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMER, F.
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: SCHEIFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
RECISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECHMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFRAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; InmEDIATE SOURCE: CLONE: pTZgpt-F18 US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 6; Conserva
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Best Local S:
Matches 6
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Query Match 5.6%; Score 53; DB 2; I Best Local Similarity 98.1%; Pred. No. 5.4e-06; Matches 53; Conservative 0; Mismatches 1;
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FILING DATE: 06-OCT-1994

APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELEPRANE: (202)293-7060
TELEPRANE: (202)293-706
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; Sequence 13, Application US/09269617
; Patent No. 6204253
; GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1025 base pairs
TYPE: nucleic acid
STRANDEDNESS: alingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LIBRARY: Human cDNA library; CLONE: SZ33
US-09-269-617-13
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
CELL TYPE: B-lymphocyte
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
172..648
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-08-795-303-1
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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APPLICANT: Anderson, Paul J.

APPLICANT: Tian, Qingsheng
APPLICANT: Tian, Qingsheng
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCES. 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, NW Suite 800
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppdidisk

COMFUTER: IBM PC compatible

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENY APPLICATION DATE: 04-FEB-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/318,947
                                                                                        CAPTIES 2003

CAPTIES 1003

CAPTIES 1003

MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,947A
FILING DATE: 06-OCT-1994

PLING APPLICATION 135
PROR APPLICATION NUMBER: 08/031,530
FILING DATE: 07-OCT-1993
ATTONENTY/AGBAT INPORMATION:
NAME: MACK, SUSSI 30,951

REGISTRATION NUMBER: 30,951

REGISTRATION NUMBER: 30,951

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERRAK: (2021293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.6%; Score 53; DB 1; Best Local Similarity 98.1%; Pred. No. 5.4e-06; Matches 53; Conservative 0; Mismatches 1
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Patent No. 5948656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (202)293-2920
TELEX: 6491103
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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172..648
             Washington
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                                                         USA
                                                       COUNTRY: U
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LOCATION:
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                                                                                                                                                                                                                                                        APPLICANT:
TITLE OF INVENTION: FACTORS THAT INTERACT WITH ONCOPROTEINS
NUMBER OF SEQUENCES: 14
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/269,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1025;
Length 1206;
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Sequence 1318, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

TITLE OF INVENTION: Mysococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 ATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCATCT 86
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51.5%; Pred. No. 0.0034;
tive 0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.0%; Score 47.2; DB 4; Length 4 Best Local Similarity 69.6%; Pred. No. 0.0002; Matches 64; Conservative 0; Mismatches 28; Indels
                                                         GENERAL INCORNATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET.054PR2;
CURRENT APPLICATION NUMBER: US/09/621,976;
CURRENT FLILMS DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335;
SOPTWARE: Patent.pm
SEQ ID NO 2061
LENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 GCGATGTGAGGAAAGGCACCTCCACCAGAAAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 eccarcrecegaacececrecececeana 220
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| LOCATION: (1)..(614)

| THER INDEMATION: unsure at all n locations

US-09-902-540-1318
                ; Sequence 2061, Application US/09621976; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

CCATION: 32

COCATION: n=a, g, c or t

US-09-621-976-2061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 51.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 65..265
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US-09-621-976-2061
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US-08-520-678A-29/c

Sequence 29, Application US/08520678A

Sequence 29, Application US/08520678A

Patent No. 5874565

GENERAL INFORMATION:

APPLICANT: Rice, Charles M.

APPLICANT: Kolykhalow, Alexander A.

TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS

TITLE OF INVENTION: C VIRUS GENOWE AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Forsyth Blvd., Suite 1400
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                                                                                                      305 ATTCTGAAAGATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 CCCCCTAAAAAGGAGAAAGAAGGAGAAAGTTGAAAAAGCAGGACAAAGAGAAAACCTGAGAAA
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4.4%; Score 42; DB 2; Length 260;
Best Local Similarity 55.5%; Pred. No. 0.0062;
Matches 81; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 TCTGACATTCTGAAAGATCCTCCTAG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION: 536

TLING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Hendersor, Melodie W.
REGISTRATION NUMBER: 37,848

REFERENCE/DOCKET NUMBER: 6029

TELECOMMUNICATION: INFORMATION:
TTELECOMMUNICATION:
TTELECOMMUNICATION:
TTELECOMMUNICATION:
TTELECOMMUNICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                         365 ACCAGCGAAACAAA 378
                                                                                                                                                                                                                                                         599 AAAAAAGACAAAA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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Sequence 11247, Application US/09248796A

Sequence 11247, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: WORD DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WORDER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PEPLICATION NUMBER: US 60/074,725
PRIOR PELING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 11247

LENGTH: 891

LENGTH: 891
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TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AAAAGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAAGACAAGG
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4.4%; Score 41.2; DB 4; Length 891;
Best Local Similarity 79.0%; Pred. No. 0.025;
Matches 49; Conservative 0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
4.4%; Score 41.8; DB 4; Length 612;
Best Local Similarity 50.2%; Pred. No. 0.013;
Matches 103; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                NAME/KEY: unsure
! LOCATION: (1)..(612)
! OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
                     FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 ACCAGCGAAACAAATCACACCTCAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-248-796A-11247
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                                                                      Sequence 29, Application US/08897126
Sequence 29, Application US/08897126
Patent No. 6297003
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
APPLICANT: Kolykhalov, Alexander A.
APPLICANT: COLYCHALOV, ALEXANDER A.
APPLICANT: KOLYCHALOV, ALEXANDER A.
APPLICANT: KOLYCHALOV, ALEXANDER A.
APPLICANT: KOLYCHALOV, ALEXANDER A.
APPLICANT: ALEXANDER A.
APPLICANT: ALEXANDER A.
APPLICANT: ALEXANDER A.
ADDRESSE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 CCCCCTAAAAAGGAGAAAAAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCTGAGAAA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/897,126 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 63105
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Henderson, Melodie W. REGISTRATION NUMBER: 37,848 REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinkle, Gregory J.
Slater, Steven C.
Wiegand, Roger C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.5'
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                      CITY: St. Louis
STATE: MO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-902-540-1357
                                                       US-08-897-126-29/c
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 TTAGTCCTAGTGTTACCAAGAAAATACCAACAAGAAAACCAAAACCAAAGTCTGACATTC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 ANTNINÀGGAANGANGGNGGANANANNNGGGNCCNINGAGNAANCTGGGGCAAANAAAGAAG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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4.3%; Score 40.6; DB 1; Length 704;
Best Local Similarity 48.1%; Pred. No. 0.033;
Matches 64; Conservative 0; Mismatches 69; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Four
                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
FPELLINGTH INCLIAM JOHN MARTIN
TITLE OF INVENTION: SOLATED STEALTH VIRUSES
ITTLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 831 West Fifth Street
STATE: Galifornia
COUNTRY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: a forage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIPICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: May 22, 1992
FILING DATE: May 22, 1992
FILING DATE: May 22, 1991
APPLICATION NUMBER: 07/764,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: WarPHING DATE: WARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET WUMBER: 213/301
TELECOMMULTATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERA: (213) 955-0440
TELERA: (213) 955-0440
TELERA: (213) 955-0440
TELERA: (7-3510
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 704 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
5-08-463-115-29/c
Sequence 29, Application US/08463115
Patent No. 5703221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 TNNCNAATCCNCC 345
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4.3%; Score 40.6; DB 1; Length 704;
Best Local Similarity 48.1%; Pred. No. 0.033;
Matches 64; Conservative 0; Mismatches 69; Indels
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MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 1995
CLASSIFICATION: 435
PILING DATE: June 5, 1995
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: including APPLICATION NUMBER: 07/887,502
APPLICATION NUMBER: 07/763,039
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: RAY 23, 1991
APPLICATION NUMBER: 20, 1991
ATTORNEY/AGENT INFORMATION:
REGERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-465-388-29/c
; Sequence 29, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:
    APPLICANT: WILLIAM JOHN MARTIN
    TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: ISOLATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 TGAAAGATCCTCC 321
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: US-08-465-388-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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US-UB-467-9843C-28

US-UB-467-9843C-28

Sequence 28, Application US/08467963C

Fatent No. 5968776

GENERAL INFORMATION:

APPLICANT: ENASYSHYN, MAYP

APPLICANT: ENASYSHYN, MAYP

TITLE OF INVENTION: CHIMERIC ENCODING A

TITLE OF INVENTION: CHIMERIC ENCORESS PROTECTION AGAINST

TITLE OF INVENTION: CHIMERIC ENCORESS ADDRESSES: 318

CORRESPONDENCE ADDRESS:

ADDRESSES: Sim & McBurney

STREET: Chimeric

CONFUTER: Condain

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

FILING D
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50.8%; Pred. No. 0.039;
tive 0; Mismatches 94; Indels (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEWART, Michael I
REGISTRATION UNDHER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPRONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.8<sup>a</sup>
Matches 97; Conservative
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TOPOLOGY:
US-08-467-963C-28
RESULT 15
US-08-467-963C-28
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Job time : 185.746 secs

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Search completed: September 11, 2005, 15:33:24

418 CACTGCACAGC 428 AAATCCAAAAC 772

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Sequence 12, Appl Sequence 247, App Sequence 12, Appl Sequence 570, App Sequence 10941, A Sequence 10941, A Sequence 571, App Sequence 571, App Sequence 272, A Sequence 272, A Sequence 272, A Sequence 272, A

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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TCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG 143
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91.9%; Score 870; DB 21; Length 1128;
Best Local Similarity 98.0%; Pred. No. 2.8e-241;
Matches 879; Conservative 1; Mismatches 17; Indels 0
                    4 US-10-116-016-12

4 US-10-116-016-12

4 US-10-133-247

1 US-10-220-020-12

1 US-10-20-12-1320

1 US-10-20-20-12

1 US-10-20-20-12

1 US-10-20-20-12

1 US-10-20-20-20-1

1 US-10-20-20-20-1

1 US-10-20-18-20-20-1

1 US-10-20-20-20-20-1

1 US-10-20-20-20-1

1 US-10-20-20-20-1

1 US-10-20-30-1

1 US-10-36-345A-26081

1 US-10-36-345A-28893

1 US-10-36-345A-28893

1 US-10-36-345A-28893

1 US-10-36-345A-2298

1 US-10-36-345A-2298

1 US-10-36-348A-2298

1 US-10-36-348A-2298
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Publication No. US20050112574A1

GENERAL INFORMATION:

APPLICATION INVENTION:

PILE OF INVENTION:

FILE REFERENCE: Angiogenesis PCT

CURRENT APPLICATION NUMBER: US/10/489,740

CURRENT FILING DATE: 2004-03-15

NUMBER OF SEQ ID NOS: 216

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

LENGTH: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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ORGANISM: Homo sapiens
US-10-489-740-35
JS-10-489-740-35
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Sequence 569, App
Sequence 1792, Ap
Sequence 1727, Ap
Sequence 121, App
Sequence 24859, Ap
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1: /cgn2_6/ptodata/2/pubpna/USOT_PUBCOMB.seq:*
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26: /cgn2
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-565-680-569
US-10-956-157-1792
US-10-956-157-7027
US-09-918-995-24859
US-09-864-761-4575
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Sequence 9298, Ap Sequence 80472, A Sequence 120013,

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Sequence 1549, Ap Sequence 35185, A Sequence 20826, A P Sequence 20844, A Sequence 12263, A Sequence 25954, A Sequence 26081, A Sequence 26081, A Sequence 26081, A Sequence 28883, A Sequence 28884, A Sequence 2

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                                              Score 868.4; DB 21; Length 1036;
Pred. No. 7.8e-241;
1; Mismatches 18; Indels 0;
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8-10-956-157-1792
; Sequence 1792, Application US/10956157
; Publication No. US20050118625A1
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ilarity 97.9%;
Conservative
 ; TYPE: DNA
; ORCANISM: Homo sapiens
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Publication No. US20050095592A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America as represented by APPLICANT: The Government of the United States of America as represented by APPLICANT: The Government of the Department of Health and Human Services APPLICANT: Diazeri, Amir A. APPLICANT: Diazeri, Amir A. APPLICANT: Liu, Edison T. TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THER FILE OF INVENTION NUMBER: US/10/505,680

CURRENT APPLICATION NUMBER: 60/357,031

PRIOR APPLICATION NUMBER: 60/357,031

PRIOR APPLICATION NUMBER: 60/357,031

PRIOR APPLICATION NUMBER: 12002-02-13

NUMBER OF SEQ ID NOS: 822

SOFTWARE: Patentin version 3.1

SEQ ID NO 569

LENGTH: 1036
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Sequence 7027, Application US/10956157
Sequence 7027, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 7027
LENGTH: 1036
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Conservative 1; Mismatches 18; Indels 0;
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                       APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION 1
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPRENEUS: 031986-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24859, Application US/09918995
; Sequence 24859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyesey, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; RIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SEQ ID NO 24859
; LENGTH, 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1) ... (502)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24859
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Best Local Similarity 96.6%
Matches 478; Conservative
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NAME/KEY: misc_feature
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US-09-918-995-24859
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                                                                                                                                          CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACAAG 803
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                                                                                                                                                                                                                                                                                                 AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGGCAT
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                                                             AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAATCTTCTGTGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GGTTTTGGGATTGTAGCGTCTGCACCTTCAGAACAGTGCTGAAGCCTTTAAATGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2156;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodi
FILE REFERENCE: PJ20701
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 90.7%; Score 859; DB 14; 11 Similarity 97.9%; Pred. No. 6.4e-238; 879; Conservative 1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 121, Application US/10103313; Publication No. US20030082758A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-10-103-313-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-103-313-121
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LENGTH: 2156
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Best Local S
Matches 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 ATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCCTCATCCACAGTGACC 310
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Patent No. US20020077270A1

GENERAL INFORMATION:

APPLICANT ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ08

CURRENT APPLICATION NUMBER: US/09/764,848

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 719
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N: EXPRESED IN BONE MARROW, SIGNAL = 1.3

N: EXPRESED IN HEART, SIGNAL = 0.98

N: EXPRESED IN FETAL LIVER, SIGNAL = 1

N: EXPRESED IN PLACENTA, SIGNAL = 4.4

N: EXPRESED IN HELA, SIGNAL = 0.96

N: EXPRESED IN HELA, SIGNAL = 1.2

N: EXPRESED IN BT474, SIGNAL = 1.5

N: EXPRESED IN ADAIT, LIVER, SIGNAL = 1.2

N: EXPRESED IN ADAIT, SIGNAL = 1.3

N: EXPRESED IN LONG, SIGNAL = 1.3

N: EXPRESED IN LONG, SIGNAL = 1.3
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                                NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4575
LENGTH: 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.3%; Score 428.6; DB 9; Best Local Similarity 99.8%; Pred. No. 1.9e-113; Matches 428; Conservative 1; Mismatches 0;
   PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTACTCT 829
                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: MOTHER INFORMATION: EDOTHER INFORMATION: EDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-4575
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US-09-764-848-12
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SEGURACE AND SEGURATE APPLICATION UNCORDED SEGURATED SEGURATED SEGURATED SEGURATION CASES APPLICANT FRANK DAVID SEGURATED SEGURATION CASES APPLICANT FRANK DAVID SEGURATED SE
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Sequence 12, Application US/10116016

Publication No. US20030054379A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT20801

CURRENT APPLICATION NUMBER: US/10/116,016

CURRENT APPLICATION NUMBER: US/10/116,016

PRIOR Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 719
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Pred. No. 1.2e-92;
2; Mismatches 19; Indels
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                                                  LOCATION: (621)
OUTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (626)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
                                                                                                                                                      LOCATION: (643)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (658)
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OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 94.4%;
Matches 389; Conservative
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NAME/KEY: misc feature
LOCATION: (621)
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE REFERENCE: PZZOTC1
CURRENT APPLICATION NUCleic Acids, Proteins, and Antibodies
FILE REFERENCE: PZZOTC1
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 623
NUMBER OF SEQ ID NOS: 623
FILE APPLICATION NOS: 620
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.0
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           NAME/KEY: misc feature

LOCATION: (626)

NAME/KEY: misc feature

LOCATION: (626)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (643)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (658)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (712)

OTHER INFORMATION: n equals a,t,g, or c

US-10-116-016-12
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FEATURE:
NAME/KEY: misc feature
LOCATION: (621)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (626)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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1. Sequence 12. Application US/10222020

2. Bublication No. US20030175739A1

2. GENERAL INFORMATION:

3. APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

PILE REFERENCE: PT208C2

CURRENT APPLICATION NUMBER: US/10/22,020

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 10/116,016

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2000-01-17

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-06-18

PRIOR PILING DATE: 2000-06-18

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-16
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Pred. No. 1.2e-92;
2; Mismatches 19; Indels
COTTION: (643)

COTHER INFORMATION: n equals a,t,g, or c name/Kers misc feature

LOCATION: (658)

OTHER INFORMATION: n equals a,t,g, or c name/Kers: nisc feature

LOCATION: (712)

COTHER INFORMATION: n equals a,t,g, or c use-10-103-313-247
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Best Local Similarity 94.4%;
Matches 389; Conservative
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PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/25,506

PRIOR APPLICATION NUMBER: 60/251,856

PRIOR PILING DATE: 2000-09-29

PRIOR PILING DATE: 2000-12-08

PRIOR PILING DATE: 2000-12-08

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01 RELIGING DATE: 2000-08-22

RR APPLICATION NUMBER: 60/216, 647

RR APPLICATION NUMBER: 60/225, 267

RR PILING DATE: 2000-08-14

RR PILING DATE: 2000-08-14

RR PILING DATE: 2000-08-14

RR APPLICATION NUMBER: 60/216, 880

RR APPLICATION NUMBER: 60/225, 270

RR APPLICATION NUMBER: 60/225, 270

RR APPLICATION NUMBER: 60/225, 270

RR APPLICATION NUMBER: 60/221, 869

RR APPLICATION NUMBER: 60/231, 869

RR APPLICATION NUMBER: 60/231, 869

RR APPLICATION NUMBER: 60/235, 834

RR APPLICATION DATE: 2000-12-08

RR APPLICATION DATE: 2000-12-08

RR APPLICATION DATE: 2000-12-08 AFFLICATION DATE: 2000-08-13
APPLICATION NUMBER: 60/220,964
APPLICATION NUMBER: 2000-07-26 FILING DATE: 2000-10-02
APPLICATION WUMBER: 60/237,038
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370 FILING DATE: 2000-08-30 APPLICATION NUMBER: 60/224,518 APPLICATION NUMBER: 60/236,369 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/224,519 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/236,327 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/241,785 FILING DATE: 2000-07-26 APPLICATION NUMBER: 60/241,809 APPLICATION NUMBER: 60/249,299 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/244,617 FILING DATE: 2000-11-01 FILING DATE: 2000-11-01 APPLICATION NUMBER: 60/225,268 APPLICATION NUMBER: 60/231,413 APPLICATION NUMBER: 60/237,039 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/226,868 APPLICATION NUMBER: 60/234,223 FILING DATE: 2000-09-21 APPLICATION NUMBER: 60/228,924 FILING DATE: 2000-08-30 APPLICATION NUMBER: 60/234,274 2000-08-14 2000-10-20 2000-10-20 2000-09-08 2000-09-05 000-09-29 FILING DATE: 2000-09-2 2000-07-1 LING DATE: FILING DATE: LING DATE: FILING DATE: FILING DATE:

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PRIOR PELICALING DATE: 2000-09-29

PRIOR PELICALION UNDERS: 60/236, 802

PRIOR PELICATION UNDERS: 60/237, 040

PRIOR PELICATION UNDERS: 60/237, 040

PRIOR PELICATION UNDERS: 60/240, 960

PRIOR PELICATION UNDERS: 60/240, 960

PRIOR PELICATION UNDERS: 60/240, 960

PRIOR PELICATION UNDERS: 60/241, 787

PRIOR PELICATION UNDERS: 60/244, 474

PRIOR PELICATION UNDERS: 60/246, 474

PRIOR PELICATION UNDERS: 60/226, 681

PRIOR PELICATION UNDERS: 60/226, 214

PRIOR PELICATION UNDERS: 60/226, 214

PRIOR PELICATION UNDERS: 60/226, 214

PRIOR PELICATION UNDERS: 60/226, 266

PRIOR PELICATION UNDERS: 60/226, 214

PRIOR PELICATION UNDERS: 60/226, 266

PRIOR PELICATION UNDERS: 60/226, 214

PRIOR PELICATION UNDERS: 60/226, 216

PRIOR PELICATION UNDERS: 60/226, 216

PRIOR PELICATION UNDERS: 60/249, 218

PRIOR PELICATION UNDERS: 60/249, 218

PRIOR PELICATION UNDERS: 60/249, 218

PRIOR PELICATION UNDERS: 60/249, 217

PRIOR PELICATION UNDERS: 60/249, 21
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RESULT 12
US-10-505-680-570/c
Squence 570, Application US/1050580
; Sequence 570, Application US/1050580
; Publication No. US20050095592A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as represented by the APPLICANT: Jazaeri, Amir A.
; APPLICANT: Liu, Edison T.
; APPLICANT: Liu, Edison T.
; APPLICANT: Liu, Edison T.
; FILE REFERENCE: 4239-64452
; FILE REPERENCE: 4239-64452
; CURRENT APPLICATION UNMBER: US/10/505,680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 GGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGCTGAAGCCTTTAAATGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 TCTGCGATKTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCTCAGCTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 cacaacaagregeacaacagrareceaceceaceacececeraaaaaggagaagaagaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 TCTGCGATGTGAGGAAAGGCACCTCCACAGAAAACCTCGGATCAATTCTCAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNCAACAAGAGAGAACAGTATGCCACCCCACCCCCTAAAAAGGAGAAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA
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94.4%; Pred. No. 1.2e-92;
tive 2; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
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                            R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,414
R FILING DATE: 2000-09-08
R PILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/233,064
                                                                                                                                                                                                                                  R FILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/233,063

R FILING DATE: 2000-09-14

R PILING DATE: 2000-09-14

R PILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/232,399
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236 CTTCTAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTG 177
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

NN: EXPRESSED IN HEART, SIGNAL = 0.98

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1

NN: EXPRESSED IN FLACENTA, SIGNAL = 1.4

NN: EXPRESSED IN HELA, SIGNAL = 0.96

NN: EXPRESSED IN HELA, SIGNAL = 1.5

NN: EXPRESSED IN HALLOO, SIGNAL = 1.5

NN: EXPRESSED IN BATA4, SIGNAL = 1.3

NN: EXPRESSED IN BRAIN, SIGNAL = 1.3

NN: EXPRESSED IN LUNG, SIGNAL = 1.3
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                   PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 2130
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Best Local Similarity 98.7<sup>3</sup>
Matches 233; Conservative
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US-9849-R64-761-71120.
US-9918-R4-761-71120.
US-90200048763A1

GAPPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPREBENCE: 2001-05-23
FRIOR FILING DATE: 2001-05-24
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-08-03
FRIOR FILING DATE: 2000-08-03
FRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 CCAGTGCAGGGTC-AGAACAGCAGAACCAGASCAGCTCGGGGTCAGAGAG-----CACAG 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633 AATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAAATTCAAA 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.6%; Score 317.8; DB 21; Length 400; 93.5%; Pred. No. 2.5e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

LOCATION: (1)...(400)

// OTHER INDEMATION: "n" represents an unknown nucleotide

US-10-505-680-570
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                               PRIOR APPLICATION NUMBER: 60/357,031
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 822
SOFTWARE: Patentin version 3.1
SEQ ID NO 570
LENGTH: 400
CURRENT FILING DATE: 2004-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 93.5
Matches 375; Conservative
                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:

APPLICANT: Chondrogene Inc.
APPLICANT: Lidew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-12
SOFTWARE: Patentin version 3.2
SEQ ID NO 10941
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCGATGTGAGGAAAAGCCACCTCCAGAAAACCTCGGATCAATTCTCAGCTGGTGG 189
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TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis FILE REPERBNCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GGAATTCGGATCCTCGAGGCCACGAAGGCCGAAACAGTGCTGAAGCCTTTAAATGCAGCA
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US-10-085-783A-10941
; Sequence 10941, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
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NAME/KEY: misc feature
LOCATION: (29)...(29)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-10941
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NAME/KEY: misc feature
LOCATION: (8)..(8)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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Matches 240; Conservative
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ORGANISM: Human
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24.3%; Score 230.4; DB 18; Length 326;
Best Local Similarity 93.4%; Pred. No. 5.1e-56;
Matches 240; Conservative 0; Mismatches 17; Indels 0;
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; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR PILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10941
; LENGTH: 326
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4)...(4)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
LOCATION: (8)...(8)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (29)...(29)
LOCATION: (29)...(29)
OTHER INFORMATION: n is a, c, g, or t
OTHER INFORMATION: n is a, c, g, or t
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                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
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BD209971 Human tra
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AX19286 Homo sapi
BC014959 Homo sapi
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AX17417 Sequence
AX18318 Sequence
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GenCore version 5.1.6
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Match Length DB
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						ALIGNMENTS			
RES	RESULT 1							_	
LOCUS	LOCUS DEFINITION		14152 uence	5 from Patent	Pate	1131 bp nt EP1108785.	DNA lir	linear PAT	11-MAY-2001
ACC	ACCESSION VERSION	XX1	AX114152 AX114152.	H	:140311				
SOU			о варі	ens (hu	(human)				
J	OKGANISM		Eukaryota; Me Mammalia: Rut	ens 1; Metazoa; Eutheria		Chordata; Cran: Primates: Cata:	Craniata; Vertebrata Catarrhini; Hominida	Б.	uteleostomi; Homo.
REF	FERENCE	1							
, E ()	AUTHORS TITLE JOURNAL	Apoj Pat	Apoptin-a Patent: E	l-associating EP 1108785-A	ing 85-A	protein 5 20-JUN-2001			
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O Z	Query Match Best Local Matches 113	Match local Similes 1131; (r)	ty 1 ervati	00.0% 00.0%	Score 1131; Pred. No. 5 0; Mismatche	DB 6; Le: .1e-291; B 0; Inc	Length 1131; Indels 0;	Gaps 0
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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larity 99.9%; Pred. No. 1.4e-290;
Conservative 0; Mismatches 1;
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Noteborn, M.H. and danen-van Oorschot, A.A.
                                                                                                                                        /note="'AAP-1-b nucleic acid'"
                                                                  Location/Qualifiers
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/db_xref="taxon:9606"
                                           Apoptin-associating protein
Patent: WO 0116165-A 9 08-MAR-2001;
Leadd B.V. (NL)
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Matches 1130; Conserv
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AX092139.1 GI:13444366

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens Homo sapiens

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Catarrhini; Hominidae; Homo.
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ACAACAAAGACCAGCGAAACAAATCACACCTCAAGGCCCCGGCTGAAAAACGTGGACAGG
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                                         361 CCACCCCTAAAAGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGGGAGAACCTGAG
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Patent: EP 1081226-A 12 07-MAR-2001;
Leadd B.V. (NL)
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Sequence 12 from Patent BP1081226.
AX138332
AX138332.1 GI:14274288
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                     GCATCCCTGGAGAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTC
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                                   AATTGTGAAAACTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTT
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Pred. No. 1.4e-290;
0; Mismatches 1;
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/note="'AAP-1-b nucleic acid'"

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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
1. .1131
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Patent: EP 1083224-A 9 14-MAR-2001;
Leadd B.V. (NL)
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Sequence 9 from Patent BP1083224.
AX138319 GI:14274285
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Best Local Similarity 99.9%;
Matches 1130; Conservative (
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Hillman,J.L., Bandman,O., Lal,P., Yue,H., Reddy,R., Tang,T.Y., Gerstin,E.H., Patterson,C., Baughn,M.R., Azimzai,Y. and Lu,D.A.M. Human transcriptional regulator molecules
Patent: 19 2002513554-A 43 14-MAY-2002;

INCYTE PHARMACETICALS INC
OS Homo sapiens (human)

PN JP 2002513554-A/43
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by JP 200251354-A/43
pp 14-MAY-2002
pp 04-MAY-1999 JP 2000547113
pp 04-MAY-1999 US 60/084254,07-AUG-1998 US 60/095827 PR 05-MAY-1998 US 60/102745
pl JENNIFER L HILLMAN,OLGA BANDMAN, PREETI LAL, HENRY YUE, ROOPA
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PI YALDA AZIMZAI, DYUNG AINA M LU
PC C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/02, A61P43/00
PC C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68//C12P21/
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841 AATTGTGAAAACTATGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTT
                                                   901 GCATCCCTGGAGAATCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCGCCAGGATAATTTC
                                                                                               TGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACAC
                                                                                                               961 IGCTIGCCATGGGCATCTGGCCACCAAGAATTTCGCACCACGACGATTACTCTTGACAC
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/organism="Homo sapiens"
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apoptin-associating protein"
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/note="Apoptin-associating protein"
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Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
Andrews, P.A., Malsh, J.A. and Gokhale, P.A.
Axordia Limited (GB)
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                                                                                                                                                                                                                                      TAGTCCTAGTGTTACCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCT
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                                                                                                                                                                                         6; Length 1036;
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                                                                                                                                                                                         Score 1019.4; DB 6;
Pred. No. 3.5e-261;
0; Mismatches 6;
                                                                                                                     1. .1036
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/mol_type="unassigned DNA"
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                                                                                                           Location/Qualifiers
                                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 1023; Conservative
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0; Mismatches 6;
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152_ 838
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeebergy, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Mocre, T., Wax, S.I., Wang, J., Haish, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.E., Casavant, T.L.,
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Abrameon, R.D., Mullahy, S.J., Bosak, S.A., McEwant, P.J.,
McKernan, K.J., Malek, J.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Malek, J.W., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
1007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parvanch Saeedi, W. Sancos, Angelique Schnerch, Ursula Skalska, Buane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                           mRNA linear PRI 29-JUN-2004 protein, mRNA (cDNA clone cds.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1128)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                 1128 bp
Homo sapiens RING1 and YY1 binding
MGC:23015 IMAGE:4902201), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1128)
                                                                                                                                                                                                                   Homo sapiens (human)
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REFERENCE
AUTHORS
TITLE
JOURNAL
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 46 Row: e Column: 4.
Location/Qualifiers
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                                                                                                                                           Ketteman, Anuradha
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                                                                                                                                        Mark Ketteman, Anura
and Michelle Whiting
                               Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and YY1 binding protein"
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortio
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http://www.systemsbiology.org
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                                                                                                                 contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcw, K.H., Schaefer, C.F., Bhat, N.K.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecnon, M., Soares, M.B., Bonddo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnetch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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SAVNDESF"
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Tel:81-45-924-5797(ex.5797), Fax:81-45-924-5834)
Location/Qualifiers
1. .4700
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                   90.0%; Score 1017.8; DB 9; 99.3%; Pred. No. 1.1e-260; ive 0; Mismatches 7;
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1. .4700
                                                                                                          /gene="YEAF1"
199. .879
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/codon start=1
/product="YX1 and E
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Submittee of Tecnology,

Bioscience and Biotechnology; 4259 Nagatsuta-cho Midori-ku,

Yokohama, Kanagawa 226-853, Japan

(B-mail:Chiwa_Sawa@hma, harvard.edu,

URL:http://www.handa.bio.titech.ac.jp/,
                       GAAAGATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAAATGCTACAACAAAAAGACCAG
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      GAAAGATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAGACCAG
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YY1 and B4TF1 associated factor
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HOMO sapiens
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Homo sapiens YEAF1 mRNA
complete cds.
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SAVNDESF"
                                                                                                                                                                                                                                                              61 ACCATGGGGGACAAGAAGAGCCCGACCAGGCCAAAAAGACAAGGGAAACCTGCCGCAGAC
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                                                                                                                Score 1017.4; DB 9
Pred. No. 1.2e-260;
0; Mismatches 1;
                                                                                                                   90.0%;
99.9%;
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Best Local Similarity 99.9
Matches 1018; Conservative
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                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 1021)

Danen-van Oorschot, A.A.A.M., Voskamp, P., Seelen, M.C., van Miltenburg, M.H., Bolk, M.W., Tait, S.W., Boesen-de Cock, J.G., Rohn, J.L., Borsel, J. and Noteborn, M.H.

Rohn, J.L., Borsel, J. and Noteborn, M.H.

Human death effector domain-associated factor interacts with the viral apoptosis agonist Apoptin and exerts tumor-preferential cell
                                                                                                  965
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Danen-van Oorschot, A.A.A.M., Boesen-de Cock, J.G.R., Borst, J. and Noteborn, M.H.M.
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1. .1021
/gene="AAP1"
                       CGACATGTCAGCAGTCAATGATGATGATCTTTCTGAAATTGCACATGGAATTGTGAAAACTA
                                                                                                                                                                                                                 ATCTGGCCACCAAGGAATTTCGCACCCCTGACGATTACTCTTGACACTTTTATGTATTCCA
                                                                      TGAATCAGGGTATGAAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAA
                                                                                                                                                                                                                                                               TIGITITIATATGATTITCCTAACAATCATITATAATTGGATGTGCTCCTGAATCTACTIT
                                                                                                  rgaarcagggrargaaarrcaaaaccrccaccrgccargcrgcrrgcarccrggagaa
                                                                                                                                    TCTTCTGTGGACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGC
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AAP-1, a binding partner of Apoptin, induces cell death tumor cells but not in normal diploid cells
Unpublished
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Cell Death Differ. 11 (5), 564-573 (2004)
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/protein_id="AAO73587.1"
/db_xref="GI:29423711"
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Submitted (31-70A-2003) Leadd BV,
AL, The Netherlands
Location/Qualifiers
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/db_xref="taxon:9606"
/cell_type="Epstein-Ba
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Danen-van Oorschot A
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
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                                                                                                                                                                                                                                  GACATCGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCA
                                                               361 recraereaaecaaacaecaracaererecaaarecracaacaaaaecaaa
                                                                                                             TCACACCTCAAGGCCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGT
                                                                                                                                                            421 TCACACCTCAAGGCCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGT
                                                                                                                                                                                                          624 AACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATC
                                                                                                                                                                                                                                                                                                    GACATCCTCACAGAGGTCCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGCAGCTC
                                                                                                                                                                                                                                                                                                                               744 GGGGTCAGAGAGCACAGACAAGGGCTCCTTCCTCCACGCCAAAGGGCGACATGTC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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99.9%; Pred. No. 2.2e-237;
tive 0; Mismatches 1;
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PB Corporation (NY) (US)
Location/Qualifiers
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    .943
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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KTAGTSTRKFREINSQUVAQQVAQQYAPPPPFKKEKTSKTRGYOKSKPENDKEISSBVTK
KNTNKTTRPKSDILADPSEANSIGSANATTKTSETNHTSRFRLKNVDRSTAQQLAVT
VGNVTVIITDFKEKTRSSSTSSSTVTSSAGSEQONQSSSGSESTDKGSDM
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Homo sapiens apoptin-associated protein APAP1 mRNA, complete cds.
AF227959
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1 (bases 1 to 936)
1 (cheng, C.M. and Yuo, C.Y.
The chicken anemia virus protein apoptin is associated with a huma apoptotic protein, APAP1
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaohsiung Medical
807, Taiwan
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Direct Submission
Submitted (33.4M-2000) Department of Biology,
University, 100 Shih-Chuan 1st Road, Kaohsiung
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77.9%; Score 881.4; DB 6;
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Noteborn, M.H. and danen-van Oorschot, A.A.
                                                            1. .947
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Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Homo sapiens (human)

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/db_xref="taxon:9606"
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Patent: BP 1108785-A 4 20-JUN-2001;
Leadd B.V. (NL)
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/organism="Homo sapiens"
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Sequence 4 from Patent EP1108785,
AX114151
AX114151.1 GI:14031159
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                                                                        TTYGTGGCCTCGAGAGATCTATGA 947
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

6; Search time 693.404 Seconds (without alignments) 9655.591 Million cell updates/sec September 11, 2005, 03:14:16 Run on:

1 tataactatctattcgatga......tggcctcgagagatctatga 1131 Sequence:

US-09-655-109A-5 1131 Title: Perfect score:

4390206 segs, 2959870667 residues Gapop 10.0 , Gapext 1.0 Searched:

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Scoring table:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

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Listing first 45 summaries

geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as: N Geneseq 16Dec04:* geneseqn2004bs: geneseqn1990s:* geneseqn2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB ID 1129.4 99.9 1131 4 AAR55596 1129.4 99.9 1131 4 AAR55596 1129.4 99.9 1131 4 AAR57485 11019.4 90.1 1036 10 ADK61994 1019.4 90.1 1036 10 ADK61999 1017 8 90.0 4700 10 ADK61999 1018 82.7 2156 4 AAS34877 935.8 82.7 2156 10 ADC46035 881.4 77.9 947 4 AAR57184 522.4 46.2 1501 5 AAS8102 468.4 41.4 57.9 947 4 AAR57184 522.4 46.2 1501 5 AAR31674 468.4 41.4 67.9 947 4 AAR35003 436 38.5 719 4 ABK43152 427.4 37.8 429 4 AAR14743	Description	Aaf55596 Nucleotid	Aaf55405 Nucleotid	Aaf57185 Apoptin-a	Aaz52452 HTRM clon	Adk66994 Gene #84	Adk61399 Ovarian c	Acf34480 Gene enco	Add18793 Human dis	Aas34877 cDNA enco	Adc46035 Human neo	Aaf55595 Nucleotid	Aaf55404 Nucleotid	Aaf57184 Apoptin-a	Aas87102 DNA encod		Aas35003 cDNA enco	Abk43152 cDNA enco	Adc46161 Human neo	Aai14743 Probe #46	Aba56475 Human foe
Match Length DE Match Length D	ID	AAF55596	AAF55405	AAF57185	AAZ52452) ADK66994) ADK61399	ACF34480		AAS34877		AAF55595	AAF55404	AAF57184	AAS87102	ACH37647	AAS35003	ABK43152		AA114743	ABA56475
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ALIGNMENTS

Nucleotide sequence of apoptin-associating protein 1 cDNA clone b. Apoptin-associating protein; AAP; apoptosis; cell proliferation; cell death; autoimmune disease; cancer; ss. AAF55596 standard; cDNA; 1131 BP. 01-SEP-2000; 2000WO-NL000612. 99EP-00202858. (first entry) (LEAD-) LEADD BV. WO200116165-A2. 02-SEP-1999; 21-OCT-1999; Homo sapiens. 08-MAR-2001. 29-MAY-2001 AAF55596;

Danen-Van Oorschot AAAM; Noteborn MHM,

WPI; 2001-235090/24.

for New nucleic acids encoding apoptin-associating proteins useful inducing apoptosis, particularly p53 independent apoptosis, or treating cancers or autoimmune diseases.

Claim 6; Fig 2; 50pp; English.

The present sequence encodes a human apoptin-associating protein 1 (AAPI). The protein is capable of providing apoptosis. AAP polypeptides and polynucleotides are useful for inducing apoptosis, particularly when apoptosis is p53-independent. They may be used to produce pharmaceutical compositions which are used for treating a disease where enhanced cell proliferation or decreased cell death is observed, particularly in cancer or in autoimmune diseases, for diagnosing a disease related with

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TGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACAC
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aberrancies in the apoptotic process, and for cancer cancer cells or cells that are prone to cancer
                                          Score 1129.4; DB Pred. No. 3e-310; 0; Mismatches
                                           99.9%;
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961 TGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACAC
                                                                                                             TITIANGTATICCATIGITITIANATGATITITCCTAACAATCATITIANAATIGGATGTGCT
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961 TGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACAC 1020
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gene therapy; AAP-1-b; 89.
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                                              Gарв
                              Length 1131;
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            C; 254 G; 234 T; 0 U; 0 Other;
                                              Indels
                              DB 4;
                             Score 1129.4; DB Pred. No. 3e-310; 0; Mismatches
             Sequence 1131 BP; 354 A; 289
                              99.9%;
99.9%;
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Matches 1130; Conserv
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The invention provides isolated or recombinant nucleic acid (I), its functional encoding an apoptin-associating proteinaceous (AAP) substance capable of apoptosis. (I), the vector comprising (I), the host cell comprising the vector and the proteinaceous substance encoded by (I) are useful for inducing apoptosis, particularly p53-independent apoptosis, and for treating a disease where enhanced cell proliferation or decreased cell death is observed, such as cancer or an autoimmune disease. A composition comprising the nucleic acid or the AAP may further be used for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells or cells that are prone to cancer. The present sequence represents the nucleotide sequence
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1021 TTTTATGTATTCCCATTGTTTTATATGATTTTTCCTAACAATCATTATAATTGGATGTGCT
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/transl_except= (pos:1015. .1017, aa:Xaa)
/transl_except= (pos:1054. .1056, aa:Xaa)
/transl_except= (pos:1054. .1056, aa:Xaa)
/product= "partial AAP-1-b protein"
/note= "Xaa are residues encoded by stop codons"
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  cDNA clone encoding a partial AAP-1-b protein
                     Sequence 1131 BP; 354 A; 289 C; 254 G; 234 T; 0 U; 0 Other;
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                                      Score 1129.4; DB Pred. No. 3e-310; 0; Mismatches
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AAS52410-Z52474 are human transcriptional regulator molecule (HTRM)

nucleotide sequences. The HTRM protein and nucleotide sequences are

nucleotide sequences. The HTRM protein and nucleotide sequences are

captured in the preventing or treating disorders associated with decreased

expression or activity of HTRM which include cell proliferative disorders

and leuksemia; immune disorders such as AIDS, Addison's disease, diabetes

and leuksemia; immune disorders such as AIDS, Addison's disease, diabetes

mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus

erythematosus, and myasthenia gravis; infections and trauma. Antagonists

of the HTRM polypeptides are useful for treating or preventing disorders

associated with increased expression or activity of HTRMs. HTRM

polypeptides, their immunogenic fragments or oligopeptides are useful for

corcenting libraries of compounds in drug screening techniques.

polymucleotides encoding HTRM are useful for blocking the activity of HTRM.

Command associated with decreased HTRM expression. Antibodies which

specifically bind HTRM and polymucleotides encoding HTRM are useful for

disorder associated with decreased HTRM expression of HTRM, particularly

in assays that detect the expression of HTRM. Nucleotide sequences

encoding HTRM may be useful to generate hybridization probes sequence

mapping the naturally occurring genomic sequence and to detect and HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus; 88; Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment. 1021 TTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATCATTTATAATTGGATGTGCT treatment of cancer CCTGAATCTACTTTTTATAAAAGGCCTTCGTGGCCTCGAGAGATCTATGA 1131 Tang YT; Lu DAM; Y, peptides useful for diagnosis, prevention and , Reddy R, Azimzai Y,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differences in gene sequences among normal, carrier and affected individuals. Using diagnostic assays, cancer can be detected prior to appearance of clinical symptoms and thereby progression of cancer can prevented by aggressive treatment or preventive measures
                                                                                                                                                                                                                                                                                                                                                                                                 GAAAGATCCTCCTAGTGAAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAGATCCTCCTAGTGAAGCAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAG
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                                                  Sequence 3641 BP; 1081 A; 718 C; 738 G; 1104 T; 0 U; 0 Other;
                                                                     Length 3641;
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                                                                    Score 1021; DB 3;
Pred. No. 3.8e-279;
0; Mismatches 5;
                                                                      Query Match
Best Local Similarity 99.5%;
Matches 1024; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibitory RNA molecule having double stranded RNA molecules, useful manipulating the phenotype of stem cells, preferably pluripotential
                                                                                                                                                                                                                                                                                           gene; inhibitory RNA; RNAi; Notch signaling target gene; phenotype;
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                                                                                                                                                                                                                                                              Gene #84 for inhibitory RNA to manipulate stem cell phenotype.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.1%; Score 1019.4; DB 10; Lengt
llarity 99.4%; Pred. No. 5.6e-279;
Conservative 0; Mismatches 6; Indels
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13-FEB-2002; 2002GB-00003387
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                                                                                    TTATAAAA 1103
                                                                                                              TTATAAAA 1105
                                                                                                                                                                                                                                                                                                           pluripotent stem cell.
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Matches 1023; Conserv
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gene expression; primer; cancer.

US DEPT HEALTH & HUMAN SERVICES SLOAN KETTERING INST CANCER RES.

(USSH)

Liu ET

Boyd J,

Jazaeri AA,

WPI; 2003-689589/65

13-FEB-2003; 2003WO-US004688 13-FEB-2002; 2002US-0357031P

WO2003068054-A2 Homo sapiens

21-AUG-2003

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TTGTTTTATATGATTTTCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTT 1020
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the specification, and (2) comparing a similarity of the pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-like tumor. The method is useful for classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. This sequence corresponds to an ovarian cancer -related gene having an altered pattern of expression in ovarian cancer. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                           Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
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                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a pattern of expression in the ovarian tumor of several markers given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAAACCTCGGATCAA
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Pred. No. 5.6e-279;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 569; 137pp; English
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Best Local Similarity 99.4%;
Matches 1023; Conservative (
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Ovarian cancer-related DNA #554 with altered ovarian cancer expression.

(first entry)

06-MAY-2004

ADK61399

BP.

ADK61399 standard; DNA; 1036

RESULT

ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

e.g.

Vadas MA;

13-NOV-2001; 2001AU-00008838. 28-AUG-2002; 2002AU-00951032.

(BION-) BIONOMICS LTD Gamble JR, Hahn CN, 2003-354655/33 P-PSDB; ABR64205

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WO2003027285-A1. Homo sapiens

Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis; gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; ischemic limb disease; coronary artery disease; gene; de. encoding angiogenesis protein BNO98. BP. 27-SEP-2001; 2001AU-00007973. 27-SEP-2001; 2001AU-00007974. 1-OCT-2001; 2001AU-00008210. 29-OCT-2001; 2001AU-00008532. ACF34480 standard; DNA; 1128 19-SEP-2002; 2002WO-AU001282. (first entry) 15-OCT-2003 03-APR-2003 ACF34480; Gene

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The invention relates to the isolation of novel genes (ACF3446-ACF34559)

C encoding proteins (ABR64180-ABR64281) involved in the process of
  encoding proteins (ABR64180-ABR64281) involved in the process of
  enaglogenesis. The nucleic acid molecules are useful in identifying and/or
  cobtaining full-length human genes involved in an angiogenic process. The
  containing full-length human animals derived from these are useful for
  containing of candidate pharmaceutical compounds used in treating
  considerably modified non-human animals derived from these are useful for
  containing of candidate pharmaceutical compounds used in treating
  conjogenesis-related disorders. They are also useful for diagnosing,
  prognosticating or treating an angiogenesis-related disorder, which
  controlled or enhanced angiogenesis or is a disorder in which
  containing a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
  conjogenesis or is a disorder in which an expanding vasculature is of
  condulator of expression or activity of the polypeptide encoded by the
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  conclusion or activity of the polypeptide encoded by the
  conclusion or activity of the polypeptide encoded by the
  concept the gene encoding one of the novel angiogenic protein
New angiogenic genes and polypeptides, useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis cardiovascular diseases.
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0; Gaps 90.1%; Score 1019.4; DB 8; Length 1128; 99.4%; Pred. No. 5.8e-279; ive 0; Mismatches 6; Indels 0; Best Local Similarity 99.4%; Matches 1023; Conservative Query Match

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ACF34480

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                                                                                           CGAAACAAATCACACCTCAAGGCCCCCGGCTGAAAAACGTGGACAGGGGCACTGCACAGCA
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                                                          CGAAACAAATCACACCTCAAGGCCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCA
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05-OCT-2001; 2001GB-00024037.
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This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antinfinamatory, ophthalmological, antiatteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention may be useful for gene therapy. The invention and be useful for diagnosing or treating a hypoxia-regulated condition, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, glucomeogenesis, glucose sincluding processes such as glycolysis, glucomeogenesis, glucose synthesis. The disease includes cancer, ischaemic conditions, reperfusion inflammatory conditions or wound healing. The present sequence is that of a disease related protein encoding DNA sequence of the invention.
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                                                                                                                  w substantially purified polypeptide, useful for diagnosing or treal hypoxia-regulated condition, such as cancer, ischemia, reperfusion jury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
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                                Mundy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4700 BP; 1411 A; 898 C; 942 G; 1446 T; 0 U; 3 Other;
                                  Naylor S,
                                Harris RA,
                                                                                                                                                                                                     Claim 27; SEQ ID NO 224; 424pp; English.
                                Ward NR,
(OXFO-) OXFORD BIOMEDICA UK LTD
                                  Kingsman SM, White J,
                                                                WPI; 2003-290046/28.
P-PSDB; ADD18792.
                                                                                                                                                        injury, retino
wound healing
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GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG

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2000US - 0225213P

2000US - 0225214P

2000US - 0225266P

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2000US - 0225268P

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ATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCA 1034
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GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding novel human neoplastic disease associated polypeptide #111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; neoplastic disease associated polypeptide; cancer; gene therapy; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; paptroditestrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.
                                                                 CGACATGTCAGCAGTCAATGATGATGATGTTGTGAAATTGCACATGGAATTGTGAAAACTA
                                                                                                                                                         TGAATCAGGGTATGAAATTCAAAACCTCCACTGCCCATGCTGCTTGCATCCCTGGAGAA
                      CTCCTCATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCA
                                  AAS34877 standard; cDNA; 2156 BP.
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24-FEB-2000; 2000US-0180628P.
22-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0189360P.
16-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-0199076P.
18-AFR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0199123P.
28-JUN-2000; 2000US-0219866P.
30-JUN-2000; 2000US-021935P.
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08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
11-DBC-2000;
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Ruben SM Barash SC, Rosen CA,

2001-465558/50 P-PSDB; AAU21678 polypeptides and polynucleotides useful as diagnostic reagents to ose diseases or disorders associated with aberrant expression or ity of polypeptides, and for treating cancers, rheumatoid arthritis. diagnose activity Novel

Claim 4; SEQ ID NO 121; 687pp; English

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal

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CAAGGAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATA

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disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS34767-AAS35050 represent cDNA sequences encoding for the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                   Score 935.8; DB 4; Length 2156;
Pred. No. 4.9e-255;
0; Mismatches 7; Indels 1;
                                                                                                                           Sequence 2156 BP; 659 A; 465 C; 419 G; 613 T; 0 U; 0 Other;
                                                                                                                                                      82.7%;
                                                                                                                                                 Query Match
Best Local Similarity 99.2'
Matches 951; Conservative
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   TGATTTTCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAA 1103
                                                                                                                                                                                                                                                                             Neoplastic disease-associated polypeptide; gene therapy; hyperproliferative disease; cancer; autoimmune disorder; diabetes; retheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder; haematologic disorder; anaemia; thrombocytopaenia; allergic reaction; asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury; inflammatory bowel disease; robm's disease; neurodegenerative disorder; alzahimer's disease; Parkinson's disease; renal disorder; acute glomerulonephritis; end-stage renal disease; acatiovascular disorder; atherosclerosis; myocarditis; infectious disease; AIDS; cachexia; anorexia; wound healing; epithelial cell proliferation; Human; ss.
                                      901 IGATTTTCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTTATAAAAA 959
                                                                                                                                                                                                                                                 Human neoplastic disease-associated gene 111 cDNA #1
                                                                                                                                           ADC46035 standard; cDNA; 2156 BP
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2000US-0180628P.
2000US-0180628P.
2000US-0189374P.
2000US-0199076P.
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2000US-0199076P.
2000US-029867P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0216486P.
2000US-0216486P.
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24-FEB-2000; 2
22-MAR-2000; 2
117-MAR-2000; 2
119-MAY-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
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The invention relates to one of 238 disclosed human neoplastic disease-
associated polypeptides encoded by 171 disclosed cDNA sequences
(including their domains, epitopes, full-length proteins, allelic variants
or species homologues). Also included are there encoding nucleic acids, a
combinant vector comprising the nucleic acid, a recombinant host cell
comprising the nucleic acid (expressing the protein), an isolated
antibody that binds specifically to the isolated polypeptide, preventing,
treating or ameliorating a medical condition, diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject,
in a biological assay, and the gene corresponding to the CDNA sequence.
The polypeptides, polynucleotides and antibodies are useful for
a biological assay, diagnosing, prognosticating, treating or
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
canaemia or thrombocytopaenia) e.g. ischaemia-reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human neoplastic disease-associated polypeptides and polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's disease.
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Matches 951; Conservative
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                                       CAAGGAAITITCGCACCTGACGAITACICTIGACACTITIATGTATTCCATTGTATTCTTATA
                           GCATCTGCGATGTGAGGAAAGGCACCTCCACCA - GAAAACCTCGGATCAATTCTCAGCTG
                                                                            GAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAAGACAAGGAAATTAGTCCTAGT
                                                                                                                                               241 GAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAGACAAGGAAATTAGTCCTAGT
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989 GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT 1048
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\transl except= (pos: 144. .146, aa: Xaa)
\note= "Xaa is an unspecified residue; encodes AAB67553"
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/note= "Xaa is an unspecified residue; encodes AAB67557"
885. .920
                                                                           744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGGATCTGGCCACCAAG
                                                                                                                                                                                                                                                              564 CAGAGAGCACAGACAAGGGCTCCTCCCGTTCCTCCAAAGGGCGAAAGGGCGAAGGGCAG
                                                        TCAATGATGAATCTTTGTGAAATTGCACATGGAATTGTGAAACTATGAATCAGGGTATG
                                                                                                                     869 AAATTCAAAACCTCCACCTGCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGACAT
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CAGAGAGCACAGACAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteinaceous substance; cell proliferation;
protein 1; AAP-1; apoptosis; cell death; cancer;
88.
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/note= "encodes AAB67552"
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                                                                                                                                                                                                                                                                                                                                                                        TTCGTGGCCTCGAGAGATCTATGA 1131
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                                                                                                                                                                                                                                 New nucleic acids encoding apoptin-associating proteins useful inducing apoptosis, particularly p53 independent apoptosis, or treating cancers or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match
Local Similarity 97.6%; Pred. No. 9.4e-240;
hes 902; Conservative 2; Mismatches 19; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U; 4 Other;
                                                                                                                                                                         Noteborn MHM, Danen-Van Oorschot AAAM
                                                                                                                                                                                                                                                                                                 Claim 6; Fig 1; 50pp; English.
                                                                                          99EP-00202858.
                                                              01-SEP-2000; 2000WO-NL000612
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                                                                                                                                          (LEAD-) LEADD
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21-OCT-1999;
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GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATATGAT 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides isolated or recombinant nucleic acid (I), its functional encoding an apoptin-associating proteinaceous (AAP) substance capable of apoptosis. (I), the vector comprising (I), the host cell comprising the vector and the proteinaceous substance encoded by (I) are useful for inducing apoptosis, particularly p33-independent apoptosis, and for treating a disease where enhanced cell proliferation or decreased cell death is observed, such as cancer or an autoimmune disease. A composition comprising the nucleic acid or the AAP may further be used for diagnosing a disease related with aberrancies in the apoptotic process, and for detecting the presence of cancer cells or cells that are
                                                                                                                                                                                                                                                                           744 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCACGAG
                     804 GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptin-associating protein, AAP; apoptosis, p53; cell proliferation, cell death, cancer; autoimmune disease; cytostatic, immunosuppressive, gene therapy; AAP-1-a; ss.
TCAATGAAACTTGTGAAATTGCACATGGAATTGTGAAAACTATGAAATCAGGGTATG
                                                                                            684 AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGACAT
                                                                                                                              CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG
                                                              AAATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCCTGGAGAATCTTCTGTGGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AAP) -1-a nucleotide sequence
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                                                                                                                                                                                          Novel isolated or recombinant apoptin-associating proteinaceous substance, apoptin-associating protein 1, useful for inducing apoptosis for treating cancer or autoimmune diseases caused by aberrant apoptosis.
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                                                                                                                              WPI; 2001-219813/23.
P-PSDB; AAB67552, AAB67553, AAB67554, AAB67555, AAB67556, AAB67557.
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Pred. No. 9.4e-240;
2; Mismatches 19;
                                                                                                                                                                                                                                                            Claim 4; Fig 1; 29pp; English
                                 99EP-00202858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.9%;
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Best Local Similarity 97.6
Watches 902; 'Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             and autoimmune diseases
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 07-MAR-2001
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prone to cancer. The present sequence represents the nucleotide sequence of the AAP-1-a cDNA clone
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                                                                                     Gaps
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                                                             Length 947;
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                                    Sequence 947 BP; 309 A; 238 C; 198 G; 198 T; 0 U;
                                                                                      19;
                                                              DB 5;
                                                          Score 881.4; DB 5;
Pred. No. 9.4e-240;
2; Mismatches 19;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclootides are also used in diagnostics as expressed sequence tags for identifying expressed conditions as expressed sequence tags for identifying expressed conditions. (II) is useful in gene therapy techniques to restore normal consistent of genes. (I) is useful in gene therapy techniques to restore normal consistent of generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and (II) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in a functions of mutations caid sequences. Assetly sor other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Assetly-Assays, a represent novel human disquestic coding sequences of the invention. Note: The sequence data for this content did not appear in the printed specification, but was obtained in the first of the content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
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46.2%; Score 522.4; DB 5; Length 1501;
Best Local Similarity 85.5%; Pred. No. 1.5e-137;
Matches 931; Conservative 0; Mismatches 97; Indels 61;
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novel human diagnostic protein #22906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 22906; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                           ATTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCCACCACCCCCTAAAA 373
-CCATCCATGACCATGGGCGACAAGAAGAGCCCGACCAGGCCAAAAAGACAAGGCGAAACC 123
                                                                                                                                                                                           TGGCCACCAAGGGATTTTCGGCACCCTGACGATTACTCTGGACACTTTTAATGTATTCCA
                                       TGCCGCAGACGAAAGGGTTTTGGGATTGTAGCGTCTGCACCTTCAGAAACAGTGCTGAAGC
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polymeptide comprising a sequence corresponding to included is a purified polymeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences in diagnostics as expressed sequence tags (EST) for in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations of the number of the sequence of the sequence is useful for generating antibodies specific for it. The present sequence is no of the 38043 isolated cDNA/EST sequences. Note: The sequence data of the third formular of the printed specification, but was not the present of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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                                                                                                                                    ss; sequencing by hybridisation; SBH; emapping; biodiversity; genetic disorder
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8 reacearracitie soz	Db 488	
2 TGACGATTACTCTTG 1016	Qy 1002	•
8 AIGCIGCCAGGATAATTICIGCITGCCAIGGGCCAICTGGCCACCAAGGAATTICGCACCC 487	Db 428	-
942 ATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCC 1001	Oy 94	Ŭ
368 CCACCTGCCCATGCTTGCATCCCTGGAGAATCTTCTGTGGACATCGACCTCTTAGTG 427	Db 36	П
2 CCACCTGCCCATGCTGCTTGCATCCCTGGAAAATCTTCTGTGGACATCGACCTCTTAGTG 941	Oy 882	~
8 TITCTGAAATTGCACATGGAATTGTGAAAACTATGAATTCAGGGTATGAAATTCAAAACCT 367	Db 308	I
2 ITTGTGAAATTGCACATGGGAATTGTGAAAACTATGAATCAGGGTATGAAATTCAAAACCT 881	Oy 822	•
8 CAAGGGCTCCTCCCCGTTCCTCCACGCCCAAAGGCCGACATGTCAGCAGTCAATGATGAATC 307	Db 248	1
2 CAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTGAGCAGTCAATGATGATGAATC 821	Oy 762	•
188 GACCTCCAGTGCAGGATCAGAACCAGAGCAGCTCGGGGTCAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	Db 18	-
2 GACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGCAGCTCGGGGTCAGAGAGCAGCAGA 761	Oy 702	_

Search completed: September 11, 2005, 10:36:38 Job time : 697.404 Becs

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Run on:

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Database

Result Š Sequence:

us-09-655-109a-5.rst

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CK230944 895 bp mRNA linear EST 09-DEC-2003 ILLUMIGEN MCQ 1331 Katze MMPL2 Macaca mulatta cDNA 5' similar to human RYBP (Hs.7910), mRNA sequence.
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/lab_host="B. coli SOLR"
/clone lib="Katze MWEL2"
/note="Organ: placenta; Vector: Uni-ZAP XR; Site_1: EcoR
1; Site_2: Xho 1; Created from Stratagene ZAP-CDNA
Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning Kit (Catalog #200450)"
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 895)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
11lumigen Biosciences Inc.
2023 Airport Way S, Suite 450, Seattle, WA 98134, USA
7el: 2063780400
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Sequenced on 2003.10.17.765 Q20 bases. Assembles in contig w/ 1
member(s). Contig contains 1 (0%) lib members.
FOR PRAIMERS
FORWARD: CCCTCACTAAAGGGAACTAAA
BACKWAARD: CCTCACTAAAGGGAATTGGGTA
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Plate: CL000013 row: C column: 06
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA=Yes.

    .895
    /organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"

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/sex="male"
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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         Score 862.2; DB 7
Pred. No. 1.8e-223
0; Mismatches 8
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Best Local Similarity 99.1%;
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AK033024 1436 bp mRNA linear HTC 03-APR-2004 Mus musculus 11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:7030405H07 product:RING1 and YY1 binding protein, full insert sequence.

RESULT 2 AK033024 LOCUS DEFINITION

ACCESSION

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G. (Dases 1 to 1336)

B. Adachi,J., Aziawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hiramoto,K., Hiraoka,T., Hirozane,T., Hayashida, K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishhi,Y., Kondo,S., Konno,H., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,A., Murata,M., Ohasto,M., Okazaki,Y., Saito,R., Saito,R., Sato,C., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sano,H., Sasaki,D., Shibata,K., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Direct Submission

L. Submitted (16-UJL-201) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (8-mail:genome-resegescriken:jp, UKL:http://genome-gsc.riken:jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1436)
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                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FANTOM Consortium. Functional a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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AK033024.1 GI:26328784
HTC; CAP trapper.
Mus musculus (house mouse)
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AJ816315
AJ816315 KN206 Bos sp. cDNA clone C0005210ill, mRNA sequence. AJ816315
AJ816315
AJ816315.1 GI:51883791
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Genomics and Genetics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
VO.020425... Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(5K+) R. Site
1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
constructed from pooled monocytes from Bos taurus (Holstein) and
Bos indicus (Sahiwals) cattle subjected to various stimuli,
including infection with the protozoan parasite Theileria annulata.
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/cell_type="bovine monocyte"
/clone_lib="KN206"
/note="Vector: pBluescriptII(SK+); Site_1: EccRV(lost);
Site_2: Not!; Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/organism="Bos sp."
/mol_type="mRNA"
/db xref="taxon:29061"
/clone="C0005210i11"
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McGuire, K. and Glass, E.J.
Unpublished ESTs, McGuire
Unpublished (2004)
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DVKKTTRKTRKPRINSQLYAQVYAQVATPPPFKEKKKKKKKKFRPPKEKPEKDKUSTSPSV
DVKKTTRKTRKPREPRILKDPPSEANSIQSANATTKTSETNHTSRPLKVVDRSTRQQLA
VTVGNVTVIITDPFKEKTRSSSTSSSTVTSSAGSEQQNQSSGGSESTDKGSSRSSTPKG
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                   /note="unnamed protein product; RING1 and YY1 binding protein (MGD|MG1:1929059, GB|NM_019743, evidence: BLASTN, putative"
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ilarity 91.6%; Pred. No. 1.4e-221;
Conservative 0; Mismatches 81;
                                                                              'db_xref="FANTOM_DB:7030405H07"
'db_xref="taxon:10090"
'clone="7030405H07"
                                                                                                                                                                                                                                                                                  /proteIn_id="BAC28131.1"
/db_xref="GI:26328785"
                               'organism="Mus musculus"
location/Qualifiers
                                              mol_type="mRNA"
strain="C57BL/6J"
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/note="putative"
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(Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
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                                           73.1%; Score 826.8; DB 1; Length 932; larity 95.2%; Pred. No. 8e-214; Conservative 0; Mismatches 42; Indels 2
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4390
Fax: 402 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stone, R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.Z., Whith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Eatas, W. War, Engereid, W. W., Rohrer, G.E., Heaton, M.P., Laegreid, W. W., Rohrer, G.B., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From testis, thymus,
semitendomosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799 AAACCTCGGATCAATTCCCAGCTGGTGGCACAGCAAGTGGCCCAGCAGTATGCCACTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 AAACCTCGGATCAATTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CCACCCCTAAAAAGGAGAAGAAGAAGGAGAAAAGTTGAAAAAGCAGGACAAAAGAGAAAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGACAAGGAAATTAGTCCTAGTGTTACCAAGAAAATACCAACAAGAAAACCAAACA
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CK/74847 11near
963641 MARC 2BOV Bos taurus CDNA 3', mRNA sequence.
CK774847
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ilarity 95.1%; Pred. No. 2e-186;
Conservative 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .799
/organism="Bos taurus"
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/db_xref="taxon:9913"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/u.x.til="caxum:jour"
/(ione="UTC-ECI-acc-m-16-0-UI"
/tissue_type="Lung"
/dev stage="Adult and Fetal"
/dev stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/lone_lib="UT-CF-ECI"
/lone_lib="UT-CF-ECI"
/note="Organ: Lung; Vector: pT7T3-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
U.CF-ECI is a normalized_cDNA library containing the UI-CF-ECI is a normalized cDNA library containing the UI-CF-ECI is a normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT7T3-Pac vector: The oligonucleotide used to prime the synthesis of first-terrand cDNA contains a library tag sequence that is located between the Not I site and the anaryments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 708.6; DB 5;
Pred. No. 1.2e-181;
0; Mismatches 4;
                                                       /mol_type="mRNA"
/db xref="taxon:9606"
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"
                                       organism="Homo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%;
ilarity 99.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Matches 711;
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                        source
    FEATURES
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UI-CF-EC1-acc-m-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-acc-m-16-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            960 CIGCITGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCCTGACGATTACTCTTGACA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020 CTTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATCATTTATAATTGGATGTGC 1079
                                                                                                                                                                                                                                                                                                 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                       840
                                                                                                                                                                              320
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Bukaryogia...

Bukaryogia...

Bukaryogia...

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo...

Hobases I to 7365

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
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                                                                                  199 GCACCCCTGGGAAATTTTCTGTGGACATCGACCTTTTAGTGATGATGCTGCCAGGATAATTT
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GAACAGCAGAACCAGAGCAGCTCGGGGTCAGAGAGACAAGAGCTCCTCCCGTTCC
                                                                                                                                                                              GAACAGCAGAACCAGAGCAGCTCGGGGGGGGGCACAGACAAGGGTTCCTCCCGCTCC
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Fax: 319 356 7171
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The following repetitive elements were found in this cDNA
agequence: 1-23, AT_rich#Low_complexity
Seg primer: M13 FORWARD
POLYA=Yes.
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Genome Res. 6 (9), 791-806 (1996)
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ISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 936)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Produrement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM53 row: c column: 12

High quality sequence stop: 713.
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GTTGGCAGTAACTGTGGGCAACGTCACCGTCATTATCACAGACTTTTAAGGAAAAAGACTCG
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E 1 (bases 1 to 906)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

NA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://mage.llnl.gov

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// organism="Homo sapiens"
// organism="MRNA"
// db_rref="taxon:9606"
// db aref="taxon:9606"
// clone="INAGE:561840"
// lab hoft="DH10B"
// lab hoft="NIH MGC 95"
// lab hoft="NIH MGC 95"
// lab hoft="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sal1-XhoI (gtcgag); Oligo-dT primer using primer
// stryrryrryrryryrva-3, size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                GAATTTCGCACCCTGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGAT 1048
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              186 CGACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAG 127
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 707)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact sigenasupport@jouy.inra.fr
                                                                                                                                                                                                                                                                                                                                             Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F. A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
                                                                                                                    NS224636 Tinear EST C
BX924636 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0017d.d.20 Sprim, mRNA sequence.
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Score 671.8; DB 5;
Pred. No. 1.3e-171;
0; Mismatches 22;
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Location/Qualifiers
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larity 93.3%; Pred. No. 8.6e-172;
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musina;

Mational institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution can be found through the I.M.A.G.E. Consortium/LINL at:
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GGCAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCCTCGACATCC 300
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/db_xref="taxon:10090"
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/dsue type="whole brain"
/dev_stage="embryo 12.5dpc"
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/clone lib="NIH BMAP FOU"
/note="organ: Brain; Vector: pXx- Asc; Site_1: EcoR I;
                                                         TCATCCACAGAGTACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAAGCAGAGCAGCTCGGGGTCG
                                                                                                                                 GAGAGCACAGACAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAGTA
                                                                                                                                                                                                        AATGATGAATCTTTCTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAA
                                                                                                                                                                                                                                                                                                                                                     ACCTCTTAGTGATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGA
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                                    TCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGCAGCTCGGGGTCA
                                                                                                            GAGAGCACAGACAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGACATGTCAGCAGTC
                                                                                                                                                                                   AATGATGAATCTTTGTGAAATTGCACATGGAATTGTGAAAACTATGAATCAGGGTATGAA
                                                                                                                                                                                                                                                            ATTCAAAACCTCCACCTGCCCATGCTGCTTGCATCCTGGAGAATCTTCTGTGGACATCG
                                                                                                                                                                                                                                                                                 ATTCACATTCTCCACCCGCCCATGCTGCTCGCATCCTGGGAATCTTCTGTGGACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The following repetitive elements were found in this cDNA sequence: 38-78, >GC_rich#Low_complexity
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTAACAATCATTTATAATTGGATGTGCTCCTGAATCTACTTTTTA 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU704183.1 GI:23632051
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Site 2: Not I; The library was constructed according Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarces gel. First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGCC. This library was created for the University Iowa Brain Anatomy Project (BMAPP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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ö 138 318 438 378 498 198 258 198 318 258 378 438 558 498 618 558 678 618 738 678 798 738 78 79 TCCATGACCATGGGCGACAAGAAGAGCCCGACCAGGCCAAAAAGACAAGGGGAAACCTGCC AGCTCGGGGTCAGAGAGACAAGGGCTCCTCCCGTTCCTCCACGCCAAAGGGCGAC gaccecerrererereaececececececerereeecececeeecece TCCATGACCATGGGCGACAAGAGACCCGACCAGGCCAAAAAAGACAAGCGAAACCTGCC 139 GCAGACGAAGGCTTTTGGGATTGTAGCGTCTGCACCTTTAGGAACAGCGCCGAAGCCTTT AAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCCACCAGAAAACCTCGGATCAATTCT AAATGCAGCATCTGCGATGTGCGGAAAGGCACCTCCACCAGGAAACCTCGCATCAATTCT AAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAAACCGTGAGAAAAGACAAGAAATTAGT CCTAGTGTTACCAAGAAAATACCAACAAGAAAACCAAACCAAAGTCTGACATTCTGAAA GATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAA GATCCTCCTAGTGAAGCTAACAGCATACAGTCTGCTAACGCTACAACAACAAAGACCAGCGAA 559 ACAAATCACACCTCAAGGCCCCGGCTGAAAACGTGGACAGGAGCACTGCACAGCAGTTG GCAGTAACTGTGGGCAACGTCACCTTATCACAGACTTTAAGGAAAAAGACTCCC TCATCGACATCCTCATCCACAGTGACCTCCAGTGCAGGGTCAGAACAGCAGAACCAGAGC AGCTCGGGCTCAGAGAGACAAAGGCTCCTCCGCTCCTCCACGCCANAGGGCGAC GCAGACGAAGGGTTTTGGGATTGTAGCGTCTGCACCCTTCAGAAACAGTGCTGAAGCCTTT Gaps ö ATGTCAGCAGTCAATGATGAATCTTTGTGAAATTGCACATGGAATTGTGAAA Score 668.6; DB 5; Length 798; Pred. No. 1e-170; 0; Mismatches 65; Indels 0 Query Match
Best Local Similarity 91.6%;
Matches 707; Conservative 0 319 619 619 79 139 199 499 13 199 259 319 379 439 379 499 439 619 619 739 799

ATGTCAGCAGTGAATGATGATCTTTCTGAGATTGCACATGGAATTGTGACA

506 552 566 612 626 670 989 729 746

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Smath, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Badas, B., Wary, J.B., White, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Guackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730 AACCAGA - GCAGCTCGGGGTCAGAGCACA - GACAAGGGCTCCTCCCGTTCCTCCACG 786
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                CTCGCTCC-TCATCGACATCCTCACAGAGACCTCCAGTGCAGGGTCAGAACAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAAGATCCTCCTAGTGAAGCAAACAGCATACAGTCTGCAAATGCTACAACAA-AGACC
                                                                                                                                        507 IGAAAGAICCICCIAGIGAAGCAAACAGCATACAGICIGCAAAIGCIACAACAACAGACC
                                                                                                                                                                                                AGCGAAACAAATCACACCTCAAGGCCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAG
                                                                                                                                                                                                                                                                                                   CAGTTGGCAGTAACTGTGGGCAACGTCACCGTCA-TTATCACAGACTTTAAGGAA-AAGA
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Plate: 120 row: A column: 12
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC_2BOV"

    .726
    /organism="Bos taurus"

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Bos taurus
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CK777039/c
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/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: potgo-dry priming.
/note="Organ: muscle; Vector: potgo-dry priming."
/note: potgo-dry priming."
/note: potgo-dry priming."
/note: potgo-dry priming.
/note: potgo-dry pr
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                        BG827273 870 bp mRNA linear EST 22-MAY-2001
602749436F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4902201 5',
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Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.linl.gov
Plate: LLCM1798 row: h column: 10
High quality sequence stop: 774.
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                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
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Mammalia; Butheria;
1 (bases 1 to 870)
MHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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ilarity 96.5%; Pred. No. 3.8e-168;
Conservative 0; Mismatches 19;
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/organism="Homo sapiens"
                                                                                                                             BG827273.1 GI:14174860
                                                                                                                                                                                sapiens (human)
                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                        mRNA sequence.
BG827273
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Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Fockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CCTGAGAAAGACAAGGAAATTAGTCCTAGTGTTACCAAGAAAATACCAACAAGAAAACC
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    Mammalia; Eutheria; Primates; Catarrhin; Hominidae; nowe.

(Dases 1 to 654)

(Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Taenebaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. A., From buman-chimp-mouse orthological control of the control 
Eutheria; Primates; Catarrhini; Hominidae; Homo
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ilarity 99.8%; Pred. No. 2.5e-166;
Conservative 0; Mismatches 1;
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14671302
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/mol_type="genomic DNA"
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VIRTUAL TRANSCRIPT, partial sequence,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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      Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                               1;
                                                                                                       Length
                                                                                                                                               Indels
                                                                                                                                                   36;
                                                                                                       Score 656.4; DB 7;
Pred. No. 2.1e-167;
0; Mismatches 36;
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genomic survey sequence
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al Similarity 94.9%;
689; Conservative
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Homo sapiens (human)
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CK299391/c
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xrefe="taxon:9606"
/clone="MAGE:5814508"
/tissue_type="Chondrosarcoma"
/dow_stage="Adult"
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/clone lib="NOI CGAP EDI"
/clone lib="NOI CGAP EDI"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: Jectoralining the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor; digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG TISSUE-chondrosarcoma
                                                                                                                                                                       BQ015219 662 bp mRNA linear BST 26-WAR-2002 UI-H-ED1-axw-f-13-0-UI.81 NCI_CGAP_ED1 Homo sapiens cDNA clone IMAGE:5834508 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/Linl at: http://image.llnl.gov

The following repetitive elements were found in this CDNA

Seq primer: M13 PORWARD

POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 AGCAAACAGCATACAGTCTGCAAATGCTACAACAAAGACCAGCGAAACAAATCACACCTC 572
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 t Dases 1 to 662)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                 828
                                                    CGTTCCTCCACGCCAAAGGGCGGACATGTCAGCAGTCAATGATGAATCTTTGTGA
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TAG_SEQ=CGTCAAGGCT"
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BQ015219.1 GI:19740120
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Homo sapiens
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Unpublished (1997)
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Fax: 319 315 9255

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Tissue Procurement: Dr. Greg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/eye.html
The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                     363
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632
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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     AAGGCCCCGGCTGAAAAACGTGGACAGGAGCACTGCACAGCAGTTGGCAGTAACTGTGGG
                                                                                                                   633 CAACGICACCGICATIAICACAGACTITIAAGGAAAAGACICGCICCTCAICGACAICCIC
                                                                                                                                                   CAACGTCACCGTCATTATCACAGACTTTAAGGAAAAGACTCGCTCCTCATCGACATCCTC
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UI-E-EJ1-ajv-e-08-0-UI.sl UI-E-EJ1 Homo sapiens CDNA clone
UI-E-EJ1-ajv-e-08-0-UI 3', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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Genome Res. 6 (9), 791-806 (1996)
97044477
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//cine=112-015-501
//cine=10rgan: eye, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-511 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed stranded cDNA was ligated to an EcoR I adaptor, digested with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
781: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Edurary Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Edurary Arrayed by: Dr. M. Bento Soares, University of Iowa
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CDNA Edurary Arrayed by: Dr. M. Bento Soares, University of Iowa
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ189224 650 bp mRNA linear EST 30-APR-2002
UI-E-EJ1-ajv-e-08-0-UI.xl UI-E-EJ1 Homo sapiens cDNA clone
                                                                                                                                                       1002 TGACGATTACTCTTGACACTTTTATGTATTCCATTGTTTTATATGATTTTCCTAACAATC 1061
   942 ATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACCC 1001
                                                          173 ATGCTGCCAGGATAATTTCTGCTTGCCATGGGCATCTGGCCACCAAGGAATTTCGCACC 114
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="UI-E-EJI-ajv-e-08-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
/tissue type="fetal Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 650)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory
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//ab_nost="DH10B (Life Technologies) (T1 phage resistant)"
//lab_nost="DH10B (Life Technologies) (T1 phage resistant)"
//clone lib="UI-B-EJ1"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UI-B-EJ1 is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand CDNA synthesis was primed
with an oligo-dT primer containing a Not 1 site. Double
stranded CDNA was ligated to an EcoR 1 adaptor, digested
with Not 1, and cloned directionally into pT7T3-Pac
vector. The oligonocleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not 1 site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
AAGCCART; optic nerve, CCATTAGAGG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).
TAG_IIB=U1-B-EJ1
TAG_ESC=AGAATCAAGA"
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optic_nerve, retina, Retina Foveal and Macular, RPE and
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sequence: 1-23, >AT rich#Low_complexity
Seq primer: M13 FORWARD
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/organism="Homo sapiens"
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AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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1177, App 60, App 60, App 61, App 68, App 1172, App 800, App 1143, App 1143, App 1163, App 117, App 11

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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Duclert, A. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REPERBENCE: 59.022.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: PATENT. PM
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                               US-09-620-312D-172
US-09-620-312D-68
US-09-620-312D-80
US-09-620-312D-799
US-09-620-312D-143
US-09-620-312D-167
US-09-620-312D-167
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US-09-620-312D-298
US-09-620-312D-332
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                                                                                                                                                                                                                                                                                                               ; Sequence 3095, Application US/09513999C; Patent No. 6783961
; GENERAL INFORMATION:
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NAME/KEY: UNSURE
LOCATION: 100
OTHER INFORMATION: Xaa=Lys or Thr
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Matches 218; Conservative
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FEATURE:
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LOCATION: 367
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LENGTH: 376
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
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                                                                                                                                                                                                                                                                                                                                                                         Issued Patents NA:*

'cgn2_6/ptodata1/ina/5A_COMB.seq:*
'cgn2_6/ptodata1/lina/5B_COMB.seq:*
'cgn2_6/ptodata1/lina/6A_COMB.seq:*
'cgn2_6/ptodata1/lina/6B_COMB.seq:*
'cgn2_6/ptodata1/lina/PCTUS COMB.seq:*
'cgn2_6/ptodata1/lina/PCTUS COMB.seq:*
'cgn2_6/ptodata1/lina/backfiles1.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-513-999C-3095
US-09-621-976-2061
US-09-20-612-11
US-09-125-12-10
US-09-12-515A-20
US-09-012-504A-20
US-09-012-504A-20
US-09-012-504A-20
US-09-6677-13
US-08-23-463-14
US-08-23-463-14
US-08-23-463-14
US-08-312-40-29
US-09-620-312D-539
US-09-620-312D-1043
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US-09-620-312D-1043
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US-09-620-312D-1043
US-09-620-312D-520
US-09-620-312D-1043
US-09-620-312D-520
US-09-620-312D-1043
US-09-620-312D-520
US-09-620-312D-906
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US-09-620-312D-627
US-09-620-312D-886
                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                1202784 seqs, 818138359 residues
                                                                                        September 11, 2005, 09:29:36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                      Post-processing; Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
                                                                                                                                                                                           IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                        US-09-655-109A-5
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Match Length
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466
1039
231
231
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1025
7218
288
1206
612
659
668
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Result

Minimum DB seq Maximum DB seq

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

184

Gaps

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10.5.0 0.6.0 10.

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Length 376; Indels 244

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FILING DAIE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/360,144
FILING DATE: 20-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFARY: 617-832-1000
TELEFARX: 617-832-1000
TELEFARX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109-2170
                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
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                                   226 CTCGACCTGTCTCCCCAGTTGGTTGCACAGCAGGTTACTCAGCAGTTTGTGCCTCCTACAC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 GCACCTTCCGGAACAGCGCCGAGGCCTTCAAGTGCATGATGTGCGATGTGCGGAAGGGCA 206
                                                                                                                                  CCAGGCCAAAAAGACAAGCGAAACCTGCCGCAGACGAAGGGTTTTGGGATTGTAGCGTCT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGCCGAAGCGGCAGCCGAAGCCGTCCTCGGATGAGGCTTACTGGGACTGTAGCGTCT 146
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CTCGGATCAATTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCCACCCCACCAC 364
                                                                                       365 CCCCTAAAAAGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAGAAACCTGAGAAAG 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.4%; Score 106.6; DB 4; Length Best Local Similarity 71.6%; Pred. No. 1.6e-22; Matches 139; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GRANET. 054 PR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                       346 GCAAAAAGAATAGCCATAAGAMAACCA 372
                                                                                                                                                                               425 ACAAGGAAATTAGTCCTAGTGTTACCA 451
                                                                                                                                                                                                                                                                                                              US-09-621-976-2061
Sequence 2061, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-269-617-11
Sequence 11, Application US/09269617;
Patent No. 620423;
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2061
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NAME/KEY: CDS
LOCATION: 65..265
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2061
LENGTH: 466
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APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFFICIAL STATEMENT SELECTION (Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.5%; Score 74; DB 3; Le:
Best Local Similarity 98.8%; Pred. No. 3.5e-12;
Matches 85; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 rrcegarcerceaegeceaegaege 105
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One Post Office Square
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/269,617
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-012-515A-20
; Sequence 20, Application US/09012515A
; Patent No. 6127521
                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
CELL TYPE: B-lymphocyte
IMMEDIATE SOURCE:
LIBRARY: Human CDNA library
CLONE: SZ29
                                                                     INFORMATION FOR SEQ ID NO: 11 SEQUENCE CHARACTERISTICS: LENGTH: 1039 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APV-036.02

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61 TATAACTATCTATTCGATGATGAAGATACCCCACCAAAACCCAAAAAAAGAGATTTGGGAAT 120
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Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels
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; Sequence 20, Application US/09012399A
; Patent No. 6503152
; GENERAL INFORMATION:
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Cottarel, Guillaume
TITLE OF ENURENCES:
NUMBER OF ENURENCES:
NUMBER OF SEQUENCES:
ADDRESSE:

                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,399A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVERTION: IMMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNIE: MA

COUNTRY: USA

IP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl NELease #1.0, Version #1.30
SOFTWARE: Patentl NELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,144A
FILING DATE: 20-DEC-1994
FLING DATE: 20-DEC-1994
FLING DATE: 20-DEC-1994
FRIENCY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: APV-036.02
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
6.5%; Score 73; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08360144A Patent No. 6150137 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 128 COTHER INFORMATION: /label= XhoI
US-08-360-144A-20
                                                                                                                                                                                           NAME/KEY: misc_feature;
; LOCATION: 128
; OTHER INFORMATION: /label= XhoI
US-09-012-515A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 rcecarcercas 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCGGATCCTCGAG 73
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Bost
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                              FEATURE
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US-09-269-617-13
; Sequence 13, Application US/09269617
: Patent No. 6204253
; GENERAL INFORMATION:
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CLONE: SZ33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1025 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-lymphocyte
                                                                                                                                                                                        61 TCGGATCCTCGAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-09-269-617-13
                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
TITLE OF INVENTION: Immunosuppressant Target Proteins
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC C-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
6.5%; Score 73; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0;
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER:
FILING DATE: 27-MAY-1994
PRIOR APPLICATION WUMBER: US 08/250,795
FILING DATE: 20-DEC-1994
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGHH: 231 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-06722-20
; Sequence 20, Application PC/TUS9506722
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 128 -
CTHER INFORMATION: /label= XhoI
US-09-012-399A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: /label= XhoI
PCT-US95-06722-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCGGATCCTCGAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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                                                                                                         1 TATAACTATCTATTCGATGATGAGATACCCCACCAAAAACGAGAATCTGGAAT
                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/269,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.3%; Score 71; DB 3; Length 1025; Best Local Similarity 92.4%; Pred. No. 2.9e-11; Matches 85; Conservative 0; Mismatches 6; Indels
Query Match
6.5%; Score 73; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 73; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10

US-08-222-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; TUTLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 TCGGATCCTCGAGGCCACGAANGCCGGCCTTC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCGGATCCTCGAGGCCACGAAGGCCTTTCTCC 92
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Sequence 29, Application US/09025151
Patent No. 6187535
                                                                     GENERAL INFORMATION:
RESULT 11
US-09-025-151-29
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; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-637-240-29
                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-025-151-29
                                                                                                                                                                                                                                                                                                                          Query Match 5.0%;
Best Local Similarity 89.7%;
Matches 61; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Conservative
APPLICANT: Legrain, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GCTTACCC 120
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Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TTGGGGGGGGGGGGGTACAGCCCATCCATGACCATGGGCGACAAGAAGAGCCCGACCAGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 CCAAAAAGACAAGCGAAACCTGCCGCAGACGAAGGGTTTTGGGATTGTAGCGTCTGCACC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 TTCAGAAACAGTGCTGAAGCCTTTAAATGCAGCATCTGCGATGTGAGGAAAGGCACCTCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 ACCAGAAAACCTCGGATCAATTCTCAGCTGGTGGCACAACAAGTGGCACAACAGTATGCC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 ACCCCACCACCCCTAAAAAGGAGAAGAAGGAGAAAGTTGAAAAGCAGGACAAAGAAAA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 CCTGAGAAAGACAAGGAAATTAGTCCTAGTGTTACCAAGAAAAATACCAACAAGAAAACC 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.2%; Score 59.2; DB 1; Length 7 Best Local Similarity 4.7%; Pred. No. 4.6e-07; Matches 19; Conservative 226; Mismatches 159; Indels
                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91 114 300.
                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                              PC-DOS/MS-DOS
                                                                    MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                            (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: pTZgpt-F18
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                      ZIP: 22313-0299
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                        USA
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Sequence 29, Application US/09637240

Sequence 29, Application US/09637240

Sequence 29, Application US/09637240

Sequence 29, Application US 6531284

GENERAL INFORMATION:

APPLICANT: Legratain, Jean-Christophe

TITLE OF INVENTION: PEAT AND EXHAUSTIVE METHOD FOR SELECTING A PREY

TITLE OF INVENTION: POLYPEPTIDE INTERACTION WITH A BAIT POLYPEPTIDE OF

TITLE OF INVENTION: INTERACTORS POLYPEPTIDES

TITLE OF INVENTION: INTERACTORS POLYPEPTIDES

TITLE OF INVENTION: INVERACTORS POLYPEPTIDES

TITLE OF INVENTION UNMBER: US/09/637,240

CURRENT FILING DATE: 2000-06-14

PRIOR PALICATION NUMBER: 09/025,151

PRIOR PILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 29

SOFTWARE PATENTION UNMBER: 2000-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: POLYPEPTIDE INTERACTING WITH A BAIT POLYPEPTIDE OF
TITLE OF INVENTION: INTERACT APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILLS REFERENCE: 03455-014
CURRENT APPLICATION NUMBER: US/09/025,151
CURRENT PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 29
LENGTH: 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56.8; DB 3; Length 288;
Pred. No. 3.4e-07;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08318947A
; Patent No. 5798245
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08795303
; Patent No. 5948656
; GENERAL INPORMATION:
    APPLICANT: Anderson, Paul J.
    APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
CORRESPONDENCES: 21
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
    STREET: 2100 Pennsylvania Avenue, NW Suite 800
    CITY: Washington
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Tian, Oingsheng
APPLICANT: Tian, Oingsheng
TITILE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
TITILE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 2.1
CORRESPONDENCES ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STRET: 2100 Pennsylvania Avenue, NW Suite 800
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPTRE: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,947A
FLING DATE: 06-OCT-1994
CLLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REGISTRATION NUMBER: 30,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 CCTCCGAGCGGCGCC 105
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(202)293-2920
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; LOCATION: 172..648
US-08-318-947A-1
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                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-795-303-1
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31 CCACCAAACCCAAAAAAAGAGATCTGGAATTCGGATCCTCGAGGCCACGAAGGCCTTTCT
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4.9%; Score 55.8; DB 2; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.7e-06;
Matches 63; Conservative 0; Mismatches 12; Indels 0
                                                                               OPERATING SYSTEM: PC-LUCK/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-CCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-CCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
RELEPHONE: (202) 293-7060
TELEPHONE: (202) 293-2920
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
10-09-620-312D-529
1 Sequence 529, Application US/09620312D
1 Patent No. 6569662
                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
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COMPUTER READABLE FORM:
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172..648
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Search completed: September 11, 2005, 15:33:26 Job time : 220.254 secs

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